Package ‘hsdar’

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Type Package

Title Manage, Analyse and Simulate Hyperspectral Data

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Suggests rgl, RCurl, pracma, foreach

Description
Transformation of reflectance spectra, calculation of vegetation indices and red edge parameters, spectral resampling for hyperspectral remote sensing, simulation of reflectance and transmittance using the leaf reflectance model PROSPECT and the canopy reflectance model PROSAIL.

License GPL

LazyLoad yes

BuildVignettes yes

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URL http://vhrz669.hrz.uni-marburg.de:8070/lcrs/, http://teledetection.ipgp.jussieu.fr/prosail/

R topics documented:

`hsdar-package` *Manage, analyse and simulate hyperspectral data in R*

Description

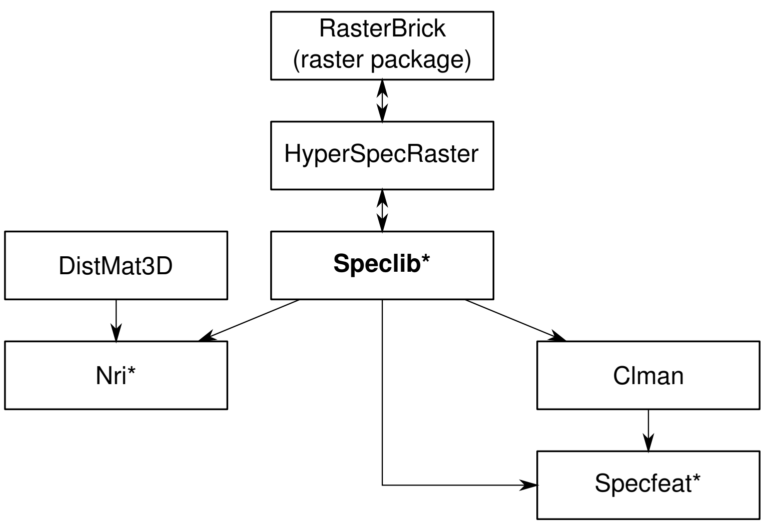
The **hsdar** package contains classes and functions to manage, analyse and simulate hyperspectral data. These might be either spectrometer measurements or hyperspectral images through the interface of **raster**.

Details

hsdar provides amongst others the following functionality.

- Data handling: **hsdar** is designed to handle even large sets of spectra. Spectra are stored in a Speclib containing, amongst other details, the wavelength and reflectance for each spectrum. **hsdar** further contains functions for plotting spectral data and applying functions to spectra.
- Data manipulation: A variety of established methods for data manipulation such as filter functions (smoothSpeclib), resampling of bands to various satellite sensors (spectralResampling), continuum removal (transformSpeclib), calculations of derivations (derivative.speclib) and extraction of absorption features (cut_specfeat) are implemented.
- Data analysis: Supported methods to analyse vegetation spectra are the calculation of red edge parameters (rededge), vegetation (vegindex) and soil (soilindex) indices as well as ndvi-like narrow band indices (nri). **hsdar** further enables to perform spectral unmixing of spectra (unmix) by use of endmember spectra.
- Data simulation: **hsdar** has implemented the models PROSAIL 5B (PROSAIL, Jacquemoud et al. 2009) and PROSPECT 5 (PROSPECT, Jacquemoud and Baret 1990) to simulate spectra of canopy and plants.

Several classes are defined and used in **hsdar**. Most of the classes are used and respective objects are created internally. However, the following figure gives an overview which class is used at which stage of processing.



Note that the asterisk marks all classes for which wrapper functions for the **caret** package exist.

To see the preferable citation of the package, type `citation("hsdar")`.

Acknowledgements

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Author(s)

Lukas Lehnert, Hanna Meyer, Joerg Bendix

---

addcp *Add fix point*

Description

Add fix point to continuum line.

Usage

```
addcp(x, ispec, cpadd)
```

Arguments

`x`	Object of class Clman.
`ispec`	ID or index of spectrum to be modified.
`cpadd`	Single value or vector of wavelength containing new fix points.

Value

Object of class `Clman` containing the updated version of x.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `deletecp`, `getcp`, `checkhull`, `makehull`, `updatecl`, `idSpeclib`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)
```

```
## Plot new line
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error
```

---

apply.DistMat3D *Apply function for class DistMat3D*

Description

Apply function to values in a 3-D distance matrix

Usage

```
## S4 method for signature 'DistMat3D'
apply(X, MARGIN, FUN, ...)
```

Arguments

X	Object of class 'DistMat3D'.
MARGIN	A vector giving the subscripts (dimensions) of the DistMat3D-object which the function will be applied over (see details).
FUN	Function to be applied. Matched with `match.fun`.
...	Further arguments passed to FUN.

Details

The specified function is either applied to the distances of all samples (MARGIN = 1) or to all distances for each sample (MARGIN = 3). In the first case, if X would be replaced by an array of same dimensions the return value would be equal if the following code is applied:

`apply(X, MARGIN = c(1,2), FUN),`

where X is an array (see examples).

Value

Depending on the length of the return value of the specified function, objects of classes numeric or matrix are returned.

Author(s)

Lukas Lehnert

See Also

`apply`, `match.fun`, `DistMat3D`

Examples

```
data(spectral_data)

## Calculate NDVI
ndvi <- nri(spectral_data, b1=800, b2=680)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)
class(nri_WV@nri)

## Calculate mean value of all samples for all indices
meanIndexVals <- apply(nri_WV@nri, MARGIN = 1, FUN = mean)
meanIndexVals

## Same but for array
nri_WV_dat <- as.array(nri_WV@nri)
meanIndexVals_arr <- apply(nri_WV_dat, MARGIN = c(1, 2), FUN = mean)

meanSampleVals <- apply(nri_WV@nri, MARGIN = 3, FUN = mean)
meanSampleVals_arr <- apply(nri_WV_dat, MARGIN = 3, FUN = mean)
```

---

apply.Speclib *Apply function for class Speclib*

Description

Apply function over all spectra or a subset of spectra

Usage

```
## S4 method for signature 'Speclib'
apply(X, FUN, byattributes = NULL, ...)
```

Arguments

X	Object of class Speclib
FUN	Function to be applied. Matched with match.fun.
byattributes	Character string giving the name of the column in the attributes to be used as subsets to apply function FUN on.
...	Further arguments passed to FUN.

Value

Object of class Speclib.

Author(s)

Lukas Lehnert

See Also

`apply`, `match.fun`, `Speclib`

Examples

```
data(spectral_data)

mean_spectrum <- apply(spectral_data, FUN = mean)
plot(mean_spectrum)

## Same as above but seperately for both seasons
mean_spectra <- apply(spectral_data, FUN = mean, byattributes = "season")
plot(mean_spectra, FUN = 1, ylim = c(0,50))
plot(mean_spectra, FUN = 2, new = FALSE)
attribute(mean_spectra)
```

---

attribute — *Handling attributes of spectra*

Description

Returning and setting attributes of spectra in Speclib or Nri.

Usage

```
## S4 method for signature 'Speclib'
attribute(object)

## S4 replacement method for signature 'Speclib,data.frame'
attribute(object) <- value

## S4 replacement method for signature 'Speclib,matrix'
attribute(object) <- value

## S4 method for signature 'Nri'
attribute(object)

## S4 replacement method for signature 'Nri,data.frame'
attribute(object) <- value

## S4 replacement method for signature 'Nri,matrix'
attribute(object) <- value
```

Arguments

`object`	Object of class `Speclib` or `Nri`.
`value`	Data frame with `nrow(value) == nspectra(object)`, or NULL.

Value

For `attribute<-`, the updated object. `attribute` returns a data frame with attribute data.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `Nri`

Examples

```
data(spectral_data)

## Returning attributes
attribute(spectral_data)
```

`bandnames` *Handling names of bands*

Description

Returning and setting names of bands in `Speclib`

Usage

```
bandnames(x)
bandnames(x) <- value
```

Arguments

`x`	Object of class `Speclib`.
`value`	Character vector of the same length as `nbands(x)`, or NULL.

Value

For `bandnames<-`, the updated object. Otherwise a vector giving the name of each band in `Speclib` is returned.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)

bandnames(spectral_data)
```

---

bdri *Band depth ratio indices*

Description

Calculate band depth ratio indices for objects of class `Specfeat`.

Usage

```
bdri(x, fnumber, index = "ndbi")
```

Arguments

x	Object of class `Specfeat`.
fnumber	Integer. Index of feature to modify.
index	Method to be applied. Currently, "bdr", "ndbi" and "bna" are available.

Details

Method "bdr" calculates the normalised band depth ratio as

$$bdr = \frac{BD}{Dc},$$

with BD is the band depth calculated by transformSpeclib and Dc is the maximum band depth called band centre. Method "ndbi" calculates the the normalised band depth index as

$$ndbi = \frac{BD - Dc}{BD + Dc}.$$

Method "bna" calculates the band depth normalised to band area as

$$bna = \frac{BD}{Da},$$

where Da is the area of the absorption feature (see feature_properties). For further information see Mutanga and Skidmore (2004).

Value

Object of class `specfeat` containing the updated version of x.

Author(s)

Lukas Lehnert and Hanna Meyer

References

Mutanga, O. and Skidmore, A. (2004): Hyperspectral band depth analysis for a better estimation of grass biomass (*Cenchrus ciliaris*) measured under controlled laboratory conditions. International Journal of applied Earth Observation and Geoinformation, 5, 87-96

See Also

transformSpeclib, define.features, specfeat

Examples

```
data(spectral_data)

## Transform speclib
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")

## Define features automatically
features <- define.features(bd)

## Isolate the features around 450nm, 700nm, 1200nm and 1500nm and
## convert to specfeat.
featureSelection <- specfeat(features, c(450,700,1200,1500))

## Plot features
plot(featureSelection,1:4)

## Calculate normalized band depth index for first feature
featureSelection_bdri <- bdri(featureSelection, 1, index = "ndbi")

## Plot result
plot(featureSelection_bdri)
```

---

cancer_spectra *Hyperspectral samples*

Description

Hyperspectral samples from the human larynx

Usage

```
data(cancer_spectra)
```

Format

An object of class `Speclib`

Details

BIANCA

Author(s)

Bianca Regeling, Lukas Lehnert

`caret::createDataPartition-methods`
Methods for Function `createDataPartition`

Description

Methods for function `createDataPartition` in package **caret**

Methods

`signature(y = ".CaretHyperspectral")` Wrapper method for `createDataPartition`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri.

`caret::createFolds-methods`
Methods for Function `createFolds` *and* `createMultiFolds`

Description

Methods for functions `createFolds` and `createMultiFolds` in package **caret**

Methods

`signature(y = ".CaretHyperspectral")` Wrapper methods for `createFolds` and `createMultiFolds`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri.

`caret::createResample-methods` *Methods for Function* `createResample`

Description

Methods for function `createResample` in package **caret**

Methods

`signature(y = ".CaretHyperspectral")` Wrapper method for `createResample`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri.

`caret::featurePlot-methods` *Methods for Function* `featurePlot`

Description

Methods for function `featurePlot` in package **caret**

Methods

`signature(x = ".CaretHyperspectral")` Wrapper method for `featurePlot`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri.

`caret::gafs` *Methods for Function* `gafs`

Description

Methods for function `gafs` in package **caret**.

Usage

```
## S4 method for signature 'Speclib'
gafs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
gafs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
gafs(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_gafs(x)
```

Arguments

x	Object of class Speclib, Nri or Specfeat. For get_gafs, x must be the output of gafs as Speclib or Nri.
y	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by setResponse is used.
cutoff	The cutoff value of the correlation coefficients between response variables.
returnData	Logical. If TRUE, the updated object of x is returned, otherwise only the result of gafs is returned.
...	Further aruments passed to gafs.

Value

If returnData == TRUE, an object of class Speclib or Nri, otherwise an object of class gafs. Note that if x is an object of class Specfeat, the function returns an object of class Speclib containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

gafs

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the attributes
spectral_data <- setPredictor(spectral_data, "season")

## Feature selection using genetic algorithms
## Note that this may take some time!
gafs_res <- gafs(spectral_data)

get_gafs(gafs_res)

## End(Not run)
```

`caret::preProcess-methods` *Methods for Function* `preProcess`

Description

Methods for function `preProcess` in package **caret**. The function is mainly internally required.

Methods

`signature(x = ".CaretHyperspectral")` Wrapper method for `preProcess`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri.

`caret::rfe` *Methods for Function* `rfe`

Description

Methods for function `rfe` in package **caret**.

Usage

```
## S4 method for signature 'Speclib'
rfe(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
rfe(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
rfe(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_rfe(x)
```

Arguments

`x`	Object of class `Speclib`, `Nri` or `Specfeat`. For `get_rfe`, `x` must be the output of `rfe` as `Speclib` or `Nri`.
`y`	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by `setResponse` is used.
`cutoff`	The cutoff value of the correlation coefficients between response variables.
`returnData`	Logical. If TRUE, the updated object of `x` is returned, otherwise only the result of `rfe` is returned.
`...`	Further aruments passed to `rfe`.

Value

If `returnData == TRUE`, an object of class `Speclib` or `Nri`, otherwise an object of class `rfe`. Note that if `x` is an object of class `Specfeat`, the function returns an object of class `Speclib` containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

`rfe`

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the attributes
spectral_data <- setPredictor(spectral_data, "season")

## Recursive feature selection
## Note that this may take some time!
rfe_res <- rfe(spectral_data)

get_rfe(rfe_res)

plot(get_rfe(rfe_res))

## End(Not run)
```

`caret::safs` *Methods for Function* `safs`

Description

Methods for function `safs` in package **caret**.

Usage

```
## S4 method for signature 'Speclib'
safs(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
safs(x, y, cutoff = 0.95, returnData = TRUE, ...)
```

```
## S4 method for signature 'Specfeat'
safs(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_safs(x)
```

Arguments

`x`	Object of class `Speclib`, `Nri` or `Specfeat`. For `get_safs`, `x` must be the output of `safs` as `Speclib` or `Nri`.
`y`	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by `setResponse` is used.
`cutoff`	The cutoff value of the correlation coefficients between response variables.
`returnData`	Logical. If TRUE, the updated object of `x` is returned, otherwise only the result of `safs` is returned.
`...`	Further aruments passed to `safs`.

Value

If `returnData == TRUE`, an object of class `Speclib` or `Nri`, otherwise an object of class `safs`. Note that if `x` is an object of class `Specfeat`, the function returns an object of class `Speclib` containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

`safs`

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the attributes
spectral_data <- setPredictor(spectral_data, "season")

## Supervised feature selection using simulated annealing
## Note that this may take some time!
safs_res <- safs(spectral_data)

get_safs(safs_res)

plot(get_safs(safs_res))
```

```
## End(Not run)
```

caret::sbf *Methods for Function* sbf

Description

Methods for function sbf in package **caret**.

Usage

```
## S4 method for signature 'Speclib'
sbf(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Nri'
sbf(x, y, cutoff = 0.95, returnData = TRUE, ...)

## S4 method for signature 'Specfeat'
sbf(x, y, cutoff = 0.95, returnData = TRUE, ...)

get_sbf(x)
```

Arguments

x	Object of class Speclib, Nri or Specfeat. For get_sbf, x must be the output of sbf as Speclib or Nri.
y	A numeric or factor vector containing the outcome for each sample. If missing, the response variable set by setResponse is used.
cutoff	The cutoff value of the correlation coefficients between response variables.
returnData	Logical. If TRUE, the updated object of x is returned, otherwise only the result of sbf is returned.
...	Further aruments passed to sbf.

Value

If returnData == TRUE, an object of class Speclib or Nri, otherwise an object of class sbf. Note that if x is an object of class Specfeat, the function returns an object of class Speclib containing the relevant transformed band values.

Author(s)

Lukas Lehnert

See Also

sbf

Examples

```
## Not run:
data(spectral_data)

## Set response variable (Chlorophyll content)
spectral_data <- setResponse(spectral_data, "chlorophyll")

## Set additional predictor variables from the attributes
spectral_data <- setPredictor(spectral_data, "season")

## Selection by filtering
## Note that this may take some time!
sbf_res <- sbf(spectral_data)

get_sbf(sbf_res)

plot(get_sbf(sbf_res))

## End(Not run)
```

`caret::setPredictor` *Set predictor variable(s)*

Description

Set predictor variable(s) to be used in functions of package **caret**.

Usage

```
## S4 method for signature '.CaretHyperspectral,character'
setPredictor(x, predictor)
```

Arguments

`x`	Object of one of the following classes: Speclib, Nri.
`predictor`	Character vector. Name of additional predictor variable(s) (from the attributes).

Value

The updated object.

Author(s)

Lukas Lehnert

See Also

`sbf`

Examples

```
## Not run:
data(spectral_data)

## Use subset of data
x <- spectral_data[c(1:31),]

## Set additional predictor variables from the attributes
x <- setPredictor(x, "season")

## End(Not run)
```

`caret::setResponse` *Set response variable*

Description

Set response variable to be used in functions of package **caret**.

Usage

```
## S4 method for signature '.CaretHyperspectral,character'
setResponse(x, response)
```

Arguments

`x`	Object of one of the following classes: Speclib, Nri.
`response`	Character. Name of response variable (from the attributes).

Value

The updated object.

Author(s)

Lukas Lehnert

Examples

```
## Not run:
data(spectral_data)

## Use subset of data
x <- spectral_data[c(1:31),]

## Set response variable (Percentage of green vegetation)
x <- setResponse(x, "PV")

## End(Not run)
```

caret::showCaretParameters *Show caret related parameters*

Description

Show caret related parameters in objects of classes Speclib, Nri.

Usage

```
showCaretParameters(x)
```

Arguments

`x`	Object of one of the following classes: Speclib, Nri.

Author(s)

Lukas Lehnert

See Also

`sbf`

caret::train-methods *Methods for Function* `train`

Description

Methods for functions `train` and `train.formula` in package **caret**

Methods

`signature(x = ".CaretHyperspectral")` Wrapper method for `train`.
Note that `".CaretHyperspectral"` is a class union containing classes Speclib, Nri.

`signature(form = "formula", data = "Speclib")` Wrapper method for `train.formula` to be used with objects of class `Speclib`.

checkhull *Check continuum line*

Description

Check if continuum line is intersecting the reflectance curve.

Usage

```
checkhull(x, ispec)
```

Arguments

x	Object of class `clman`.
ispec	ID or index of spectrum to be checked.

Value

Object of class `list`.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

transformSpeclib, addcp, deletecp, makehull, updatecl

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Check new hull
hull <- checkhull(spec_clman, 1)
```

```
hull$error

## Add fix point at 4596 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2496)

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error
```

Clman ** Clman class*

Description

Class to store and handle manual continuum lines

Usage

```
Clman(wavelength, cp, hull, spectra, outdatedhull = NULL, mask = NULL)

## S4 method for signature 'Clman'
plot(x, ispec, subset = NULL, numeratepoints = TRUE,
    hull.style = NULL, points.style = list(), ...)
```

Arguments

`wavelength`	Vector with corresponding wavelength for each band.
`cp`	Data frame or matrix containing fix points. Fix points have numbers greater than 0, all other bands are 0.
`hull`	Data frame or matrix containing linear hull.
`spectra`	Data frame, matrix of raster object of class 'SpatialGridDataFrame' with spectral data.
`outdatedhull`	Data frame or matrix containing hull of step before for undo porposes.
`mask`	Data frame with masked parts in the spectra. See `mask`.
`x`	Object of class `clman`.
`ispec`	Name or index of spectrum to be plotted.
`subset`	Lower and upper spectral limits used for plot.
`numeratepoints`	Flag if points should be numerated in plot.
`hull.style`	List of arguments passed to `lines` to construct the continuum line.
`points.style`	List of arguments passed to `points` to construct the continuum points. May be `NULL` to suppress plotting of fix points.
`...`	Further arguments passed to plot.default.

Value

Object of class Clman.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

transformSpeclib, plot

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot clman
plot(spec_clman, ispec = 1, subset = c(400, 1000))
```

---

clman *Methods to create, manipulate and query objects of class 'Clman'.*

Description

Methods to create, manipulate and query objects of class 'Clman'.

Usage

```
## Creation of objects
## S4 method for signature 'Clman'
initialize(.Object, ...)

## S4 method for signature 'Clman'
spectra(object, ...)

## S4 replacement method for signature 'Clman,data.frame'
spectra(object) <- value

## S4 replacement method for signature 'Clman,matrix'
spectra(object) <- value

## S4 replacement method for signature 'Clman,numeric'
spectra(object) <- value
```

Arguments

`.Object,object`	Matrix, numeric or array in cases of creation of 'Clman' objects otherwise object of class 'Clman'.
`value`	Object of class numeric, matrix or array which is used for replacement of the values in x.
`...`	Arguments passed to `createspeclib`.

Value

For `spectra<-`, the updated object. Otherwise a matrix returning the spectra in the Clman object.

Note

The functions to create objects of class `Clman` are mainly internally needed by `transformSpeclib`.

Author(s)

Lukas Lehnert

See Also

`dist.speclib`, `Clman`, `transformSpeclib`, `plot`

`Clman-class` ** Clman class*

Description

Class to handle continuum removal objects (extends `Speclib` class).

Details

The class extends `Speclib`s and adds two additional slots:

- cp: Object of class `matrix` containing continuum points for all spectra (rows) and bands (columns).
- hull: Object of class `matrix` containing hull lines for all spectra (rows) and bands (columns).

Note

See figure in `hsdar-package` for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `plot`

`cor.test` *Test for association/correlation between nri values and vector of samples*

Description

Test for association between paired samples (with one variable being nri-values), using one of Pearson's product moment correlation coefficient, Kendall's tau or Spearman's rho.

Usage

```
## S4 method for signature 'Nri'
cor.test(x, y, ...)
```

Arguments

`x`	Object of class `Nri` or numerical vector
`y`	Object of class `Nri` or numerical vector
`...`	Further arguments passed to `cor.test`

Details

NRI-values may be used as x and/or as y variable. If x and y are NRI-values the number of samples in both datasets must be equal. For additional information on correlation tests see details in `cor.test`.

Value

Object of class `Nri`

Author(s)

Lukas Lehnert

See Also

`plot`, `cor.test`, `glm.nri`, `lm.nri`, `getNRI`

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)
```

```
cortestnri <- cor.test(nri_WV, attribute(spec_WV)$chlorophyll)

cortestnri
```

`cubePlot` *cubePlot*

Description

Plotting 3D cube of hyperspectral data using **rgl**-package

Usage

```
cubePlot(x, r, g, b, ncol = 1, nrow = 1,
         sidecol = colorRamp(palette(heat.colors(100))), ...)
```

Arguments

`x`	Object of class `HyperSpecRaster`.
`r`	Integer. Index of band used as red channel. If omitted, the band closest to 680 nm is selected.
`g`	Integer. Index of band used as green channel. If omitted, the band closest to 540 nm is selected.
`b`	Integer. Index of band used as blue channel. If omitted, the band closest to 470 nm is selected.
`ncol`	Integer giving the column(s) in `x` which is/are used to plot the spectral dimension.
`nrow`	Integer giving the row(s) in `x` which is/are used to plot the spectral dimension.
`sidecol`	ColorRamp used to illustrate spectral dimension.
`...`	Further arguments (currently ignored)

Author(s)

Lukas Lehnert

See Also

`HyperSpecRaster`

Examples

```
## Not run:
data(spectral_data)
ras <- HyperSpecRaster(spectral_data, nrow = 9, ncol = 9)

cubePlot(ras)

## End(Not run)
```

cut_specfeat *Cut absorption features*

Description

Function cuts absorption features to a user-specified range.

Usage

```
cut_specfeat(x, ..., fnumber, limits)
```

Arguments

x	An object of class "Specfeat" containing isolated features determined by specfeat.
fnumber	A vector of the positions of the features in x to be cut.
limits	A vector containing the start and end wavelength for each fnumber. The corresponding feature will be cut to this specified range.
...	Further arguments passed to generic functions. Currently ignored.

Value

An object of class Specfeat containing the cut features.

Author(s)

Hanna Meyer and Lukas Lehnert

See Also

define.features, specfeat, Specfeat

Examples

```
data(spectral_data)

##Example to cut the features around 450nm and 700nm to a specific range
## Transform speclib
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")

## Define features
features <- define.features(bd)

## Convert speclib to specfeat giving center wavelength of features
featureSelection <- specfeat(features, c(450,700,1200,1500))

## Cut 1st and 2nd feature to [310 nm, 560 nm] and [589 nm, 800 nm]
featuresCut <- cut_specfeat(x = featureSelection, fnumber = c(1,2),
```

```
                          limits = c(c(310, 560), c(589, 800)))

## Plot result (1st and 2nd feature)
plot(featuresCut, fnumber = 1:2)
```

`define.features` *Definition of absorption features*

Description

Function sets the spectral range of absorption features.

Usage

```
define.features(x, tol = 1.0e-7, FWL = NULL)
```

Arguments

`x`	Object of class `Speclib` containing the band depth or ratio transformed reflectance spectra.
`tol`	The tolerance of the band depth which defines a wavelength as a start or end point of a feature. Usually a band depth of 0 or a ratio of 1 indicates feature limits, however, better results are achieved if slightly deviating values are tolerated.
`FWL`	Optional. If passed, result is directly converted into `Specfeat`. A vector containing one wavelength per feature to be isolated, e.g. the major absorption features. Features which include these specified wavelengths will be isolated.

Details

Absorption features are defined as the area between local maxima in the reflectance spectra. This function adds the information of the feature limits to the `Speclib`. Thus, it is a pre-processing step to isolate features.

Value

The updated `Speclib` containing additional information about the feature limits. If `FWL` is not `NULL`, result will be of class `Specfeat`.

Author(s)

Hanna Meyer and Lukas Lehnert

See Also

`transformSpeclib`, `specfeat`, `Specfeat`

Examples

```
data(spectral_data)

##Example to define feature limits
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")

## Define features
features <- define.features(bd)
```

`deletecp` *Delete fix point*

Description

Delete fix point from continuum line.

Usage

```
deletecp(x, ispec, cpdelete)
```

Arguments

`x`	Object of class `Clman`.
`ispec`	ID or index of spectrum to be modified.
`cpdelete`	Single value or vector of wavelength containing fix point(s) to be deleted.

Value

Object of class `Clman` containing the updated version of x.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `addcp`, `getcp`, `checkhull`, `makehull`, `updatecl`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)
## Mask parts not necessary for the example
mask(spec) <- c(1600, 2600)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, subset = c(1100, 1300))

## Find wavelength of fix point to be deleted
getcp(spec_clman, 1, subset = c(1100, 1300))

## Delete all fix points between 1200 and 1240 nm
spec_clman <- deletecp(spec_clman, 1, c(1200:1240))

## Plot new line
plot(spec_clman, ispec = 1, subset = c(1100, 1300))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error
```

---

derivative.speclib *Derivation*

Description

Calculate derivations of spectra

Usage

```
derivative.speclib(x, m = 1, method = "sgolay", ...)
```

Arguments

`x`	Object of class `Speclib`.
`m`	Return the m-th derivative of the spectra.
`method`	Character string giving the method to be used. Valid options are `"finApprox"` or `"sgolay"`.
`...`	Further arguments passed to `sgolayfilt`.

Details

Two different methods are available:

- Finite approximation (`finApprox`):

$$\frac{dr}{d\lambda} = \frac{r(\lambda_i) - r(\lambda_{i+1})}{\Delta\lambda},$$

  where r_i is the reflection in band i and $\Delta\lambda$ the spectral difference between adjacent bands.
- Savitzky-Golay derivative computation (`sgolay`)

Value

Object of class `Speclib`.

Author(s)

Lukas Lehnert

References

Tsai, F. & Philpot, W. (1998): Derivative analysis of hyperspectral data. Remote Sensing of Environment 66/1. 41-51.

See Also

`sgolayfilt`, `vegindex`

Examples

```
data(spectral_data)

## Calculate 1st derivation
d1 <- derivative.speclib(spectral_data)

## Calculate 2nd derivation
d2 <- derivative.speclib(spectral_data, m = 2)

## Calculate 3rd derivation
d3 <- derivative.speclib(spectral_data, m = 3)

par(mfrow=c(2,2))
plot(spectral_data)
plot(d1)
plot(d2)
plot(d3)
```

`dim.speclib` *Dimensions of Speclib*

Description

Get dimension(s) of Speclib

Usage

```
## S4 method for signature 'Speclib'
dim(x)

nspectra(x)
nbands(x)
```

Arguments

x	Object of class `Speclib`.

Value

Vector of length = 2 or single integer value.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

dim(spectral_data)
```

`dist.speclib` *Distance between spectra*

Description

Calculation of distance matrices by using one of the various distance measure to compute the distances between the spectra in `Speclib`. Spectral Angle Mapper (SAM) is calculated with `sam` giving reference spectra or with `sam_distance` taking all combinations between spectra in single Speclib into account.

Usage

```
dist.speclib(x, method = "sam", ...)

## Direct call to Spectral Angle Mapper function
sam(x, ref)
sam_distance(x)
```

Arguments

`x`	Object of class `Speclib`.
`method`	The distance measure to be used. This must be one of "sam", "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski".
`ref`	Object of class `Speclib` containing reference spectra.
`...`	Further arguments, passed to other methods.

Details

Available distance measures are "spectral angle mapper" (`sam`) and all distance measures available in `dist`. Spectral angle mapper is calculated with the following formula:

$$sam = \cos^{-1}\left(\frac{\sum_{i=1}^{nb} t_i r_i}{\sqrt{\sum_{i=1}^{nb} t_i^2}\sqrt{\sum_{i=1}^{nb} r_i^2}}\right)$$

nb is the number of bands in Speclib. t_i and r_i are the reflectances of target and reference spectrum in band i, respectively.

Value

The `dist-method` for Speclibs returns an object of class `"dist"`. See `dist` for further information on class `"dist"`. Both other functions return an object of class matrix.

Author(s)

Lukas Lehnert

References

Kruse, F. A.; Lefkoff, A. B.; Boardman, J. W.; Heidebrecht, K. B.; Shapiro, A. T.; Barloon, P. J. & Goetz, A. F. H. (1993). The spectral image processing system (SIPS) – interactive visualization and analysis of imaging spectrometer data. Remote Sensing of Environment, 44, 145-163.

See Also

dist, Speclib

Examples

```
data(spectral_data)

## Mask channel crossing part (arround 1050 nm) and strong
## water absorption part (above 1350 nm)
mask(spectral_data) <- c(1045, 1055, 1350, 1706)

## Calculate distance between all spectra from spring
## using spectral angle mapper
dist.speclib(subset(spectral_data, season == "spring"))


## Calculate spectral angle mapper between reference spectrum
## and spectral_data
## Use first spectrum from summer as reference
distance <- sam(subset(spectral_data, season == "spring"),
                subset(spectral_data, season == "summer")[1,])
```

---

distMat3D — *Methods to create, manipulate and query objects of class 'DistMat3D'.*

Description

Methods to create, manipulate and query objects of class 'DistMat3D'. The following relational operators are defined to compare values between 'DistMat3D'-object(s): `<, <=, ==, >, >=`

Usage

```
## Creation of objects
## S4 method for signature 'numeric'
distMat3D(x, ncol, nlyr)

## S4 method for signature 'matrix'
distMat3D(x, lower_tri = TRUE)

## S4 method for signature 'array'
```

```
distMat3D(x, lower_tri = TRUE)

## Conversion methods
## S4 method for signature 'DistMat3D'
as.array(x)

## S4 method for signature 'DistMat3D'
as.matrix(x, lyr = 1)

## Query of properties
## S4 method for signature 'DistMat3D'
dim(x)

## S4 method for signature 'DistMat3D'
ncol(x)

## S4 method for signature 'DistMat3D'
nrow(x)

## Manipulate and query data in objects
## S4 method for signature 'DistMat3D,ANY,ANY'
x[i, j, n]

## S4 replacement method for signature 'DistMat3D,ANY,ANY'
x[i, j, n] <- value


## S4 method for signature 'DistMat3D'
show(object)
```

Arguments

x,object	Matrix, numeric or array in cases of creation of 'DistMat3D' objects otherwise object of class 'DistMat3D'.
ncol	Number of columns in the new 'DistMat3D' object.
nlyr	Number of layer in the new 'DistMat3D' object.
lower_tri	Flag if only the lower triangle is used.
lyr	Layer in the 'DistMat3D' object to be transformed into matrix.
value	Object of class numeric, matrix or array which is used for replacement of the values in x.
i,j,n	Subscripts to access data.

Author(s)

Lukas Lehnert

See Also

DistMat3D, apply, Nri

Examples

```
data(spectral_data)

## Mask channel crossing part (arround 1050 nm) and strong
## water absorption part (above 1350 nm)
mask(spectral_data) <- c(1045, 1055, 1350, 1706)

## Calculate SAM distances (object of class 'dist')
sam_dist <- dist.speclib(subset(spectral_data, season == "summer"))

## Convert to class 'distMat3D'
sam_dist <- distMat3D(as.matrix(sam_dist))

sam_dist
```

DistMat3D-class   * *DistMat3D class*

Description

Class to store effectively (large) distance matrices (up to 3D).

Details

Object with 3 slots:

- values: Numerical vector containing distance values
- ncol: Number of columns in the 3D-matrix. Number of columns equals always the number of rows
- nlyr: Number of layers in the 3D-matrix

Note

See figure in hsdar-package for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

distMat3D

`feature_properties` *Calculation of properties of features*

Description

Function to calculate feature properties such as the area, the position of the maximum and several other parameters.

Usage

```
feature_properties(x)
```

Arguments

`x`	Object of class `Specfeat`

Details

The function calculates several parameters:

- *area*: The feature area is calculated by

$$area_{F_i} = \sum_{k=min(\lambda)}^{max(\lambda)} BD\lambda,$$

  with $area_{F_i}$ is the area of the feature i, $min(\lambda)$ is the minimum wavelength of the spectrum, $max(\lambda)$ is the maximum wavelength of the spectrum and BD is the band depth.
- *max*: Wavelength position of the maximum value observed in the feature.
- Parameters based on half-max values:
  - *lo* and *up*: Wavelength position of the *lo*wer and *up*per half-max value.
  - *width*: Difference between wavelength positions of *up*per and *lo*wer half-max values.
  - *gauss_lo*: Similarity of the Gauss distribution function and the feature values between the *lo*wer half-max and the *max*imum position. As similarity measurement, the root mean square error is calculated.
  - *gauss_up*: Same as above but for feature values between the *max*imum position and the *up*per half-max.

Value

An object of class `Specfeat` containing the properties as (part of the) attribute table.

Author(s)

Hanna Meyer \& Lukas Lehnert

See Also

define.features, specfeat

Examples

```
data(spectral_data)

## Example calculating the areas of the features around 450nm,
## 700nm, 1200nm and 1500nm.
bd <- transformSpeclib(subset(spectral_data, season == "summer"),
                       method = "sh", out = "bd")

## Define features
features <- define.features(bd)

## Convert speclib to specfeat giving center wavelength of features
featureSelection <- specfeat(features, c(450,700,1200,1500))

## Calculate properties of features
featureProp <- feature_properties(featureSelection)
```

---

get.gaussian.response *Gaussian response function*

Description

Simulate Gaussian response function for satellite sensor

Usage

```
get.gaussian.response(fwhm)
```

Arguments

fwhm	Object of class data.frame with three columns. See details and examples sections.

Details

The characteristics of the sensor must be passed as a data.frame with three columns: first column is used as name for bands, second with lower bounds of channels and third column with upper bounds. Alternatively, the data.frame may encompass band centre wavelength and full-width-half-maximum values of the sensor. Function will check the kind of data passed by partially matching the names of the data frame: If any column is named "fwhm" or "center", it is assumed that data are band centre and full-width-half-maximum values.

Value

Data frame with response values for all bands covering the entire spectral range of satellite sensor.

Author(s)

Lukas Lehnert

See Also

get.sensor.characteristics, get.gaussian.response

Examples

```
par(mfrow=c(1,2))
## Plot response function of RapidEye
plot(c(0,1)~c(330,1200), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
data_RE <- get.gaussian.response(get.sensor.characteristics("RapidEye"))
xwl_response <- seq.int(attr(data_RE, "minwl"),
                        attr(data_RE, "maxwl"),
                        attr(data_RE, "stepsize"))
for (i in 1:ncol(data_RE))
  lines(xwl_response, data_RE[,i], col = i)

## Plot original response function
data_RE <- get.sensor.characteristics("RapidEye", TRUE)

plot(c(0,1)~c(330,1200), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
xwl_response <- seq.int(attr(data_RE$response, "minwl"),
                        attr(data_RE$response, "maxwl"),
                        attr(data_RE$response, "stepsize"))
for (i in 1:nrow(data_RE$characteristics))
  lines(xwl_response, data_RE$response[,i], col = i)

## Simulate gaussian response for arbitrary sensor with 3 bands
sensor <- data.frame(Name = paste("Band_", c(1:3), sep = ""),
                     center = c(450, 570, 680),
                     fwhm = c(30, 40, 30))

## Plot response function
par(mfrow=c(1,1))
plot(c(0,1)~c(330,800), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
data_as <- get.gaussian.response(sensor)
xwl_response <- seq.int(attr(data_as, "minwl"),
                        attr(data_as, "maxwl"),
                        attr(data_as, "stepsize"))
for (i in 1:3)
  lines(xwl_response, data_as[,i], col = i)
```

get.response *Satellite response functions*

Description

Handling satellite sensor response functions

Usage

```
get.response(sensor, range = NULL, response_function = TRUE,
             continuousdata = "auto")
```

Arguments

sensor	Name or integer value of satellite sensor. Matched with get.sensor.name.
range	Vector of length = 2 containing maximum and minimum wavelength to be considered.
response_function	If TRUE, spectral response function else wise Gaussian response function will be returned.
continuousdata	Definition if returned Speclib is containing continuous data or not.

Value

Object of class Speclib containing spectral response values instead of reflectance value. Spectral response values may be accessed with spectra.

Author(s)

Lukas Lehnert

See Also

get.sensor.name, get.sensor.characteristics, get.gaussian.response

Examples

```
## See example in get.sensor.characteristics
```

get.sensor.characteristics

Sensor characteristics

Description

Get channel wavelength of satellite sensor

Usage

```
get.sensor.characteristics(sensor, response_function = FALSE)
```

Arguments

sensor	Character or integer. Name or numerical abbreviation of sensor. See 'sensor="help"' or 'sensor=0' for an overview of available sensors.
response_function	If TRUE, the spectral response function is returned

Author(s)

Lukas Lehnert

See Also

spectralResampling

Examples

```
## Return implemented sensors
get.sensor.characteristics(0)

## RapidEye
data_wv <- get.sensor.characteristics("RapidEye", TRUE)

## Plot response functions
plot(c(0,1)~c(330,1200), type = "n", xlab = "Wavelength [nm]",
     ylab = "Spectral response")
xwl_response <- seq.int(attr(data_wv$response, "minwl"),
                        attr(data_wv$response, "maxwl"),
                        attr(data_wv$response, "stepsize"))
for (i in 1:nrow(data_wv$characteristics))
  lines(xwl_response, data_wv$response[,i], col = i)
```

`get.sensor.name` *Satellite sensor name*

Description

Get satellite sensor name by integer value

Usage

```
get.sensor.name(sensor)
```

Arguments

`sensor`	Integer value to match against predefined satellite sensors.

Details

See `get.sensor.characteristics` to get overview on available satellite sensors.

Value

Name of satellite sensor as character string.

Author(s)

Lukas Lehnert

See Also

`get.sensor.characteristics`

Examples

```
get.sensor.name(1)
```

`getcp` *Get fix points*

Description

Get fix points of continuum line within spectral range.

Usage

```
getcp(x, ispec, subset = NULL)
```

Arguments

`x`	Object of class `Clman`.
`ispec`	ID or index of spectrum to be analysed.
`subset`	Vector of `length = 2` giving the lower and upper limit of spectral range.

Value

Object of class `list` containing two elements:

- ptscon: Data frame with wavelength and reflectance of fix points
- ispec: Index of analysed spectrum within passed `Clman`-object.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `deletecp`, `addcp`, `Clman`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Fix points
spec_cp <- getcp(spec_clman, 1, c(400, 800))
spec_cp
```

`getNRI` *Return nri-values*

Description

Return normalized ratio index values giving the wavelength

Usage

```
getNRI(nri, wavelength)
```

Arguments

`nri`	Object of class 'Nri'
`wavelength`	Wavelength values where nri is returned. See details section.

Details

Wavelength can be passed in three ways. As the result of nri_best_performance, as a data frame with two columns or as a vector of length 2. In the first two cases, the result will be a data frame (if data frames contain more than one row) with the nri-values of each pair of wavelengths. In the latter case it will be a vector.

Author(s)

Lukas Lehnert

See Also

nri, Nri

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Build glm-models
glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Return best 5 models
BM <- nri_best_performance(glmnri, n = 5, coefficient = "p.value")

## Get nri values for the 5 models
nri_BM <- getNRI(nri_WV, BM)
```

---

get_reflectance *Get reflectance values*

Description

Returns weighted or unweighted reflectance values at wavelength position.

Usage

```
## S4 method for signature 'Speclib'
get_reflectance(spectra, wavelength, position, weighted = FALSE,
                           ...)
```

Arguments

`spectra`	Object of class `Speclib` or data.frame with reflectance values.
`wavelength`	Vector with wavelength values.
`position`	Numeric value passing the position of reflectance values to be returned in dimensions of the wavelength values.
`weighted`	Logical indicating if reflectance values should be interpolated to fit wavelength position. If `FALSE` the reflectance values of nearest neighbour to passed position are returned.
`...`	Arguments to be passed to specific functions. For `get_reflectance.default` ignored.

Value

A vector with reflectance values for each spectrum is returned. If position falls outside of spectral range of input values, `NA` values are returned.

Author(s)

Lukas Lehnert & Hanna Meyer

See Also

`spectra`

Examples

```
data(spectral_data)
```

---

glm.nri *(Generalised) Linear models from normalised ratio indices*

Description

Build (generalised) linear models of normalised ratio indices as response and predictor variables

Usage

```
lm.nri(formula, preddata = NULL, ...)
glm.nri(formula, preddata = NULL, ...)
```

Arguments

`formula`	Formula for (generalized) linear model
`preddata`	Data frame or speclib containing predictor variables
`...`	Further arguments passed to `lm`, `glm` and generic `print.default`

Details

NRI-values may be used as predictor or response variable. If NRI-values are predictors, the models are build only with one index as predictor instead of all available indices. In this case, only one predictor and one response variable is currently allowed. See help pages for `lm` and `glm` for any additional information. Note that this function does not store the entire information returned from a normal (g)lm-model. To get full (g)lm-models use either the function `nri_best_performance` to return best performing model(s) or extract nri-values with `getNRI` and build directly the model from respective index.

See details in Nri-`plot`-method for information about plotting.

Value

The function returns an object of class `Nri`. The list in the slot *multivariate* contains the new (g)lm information which depends on the kind of model which is applied:

1. `lm.nri`: The list contains the following items:
    - Estimate: Coefficient estimates for each index and term
    - Std.Error: Standard errors
    - t.value: T-values
    - p.value: P-values
    - r.squared: R^2 values
2. `glm.nri`: The list contains the following items (depending on formula used):
    - Estimate: Coefficient estimates for each index and term
    - Std.Error: Standard errors
    - t.value/z.value: T-values or Z-values
    - p.value: P-values

Author(s)

Lukas Lehnert

See Also

`plot`, `lm`, `glm`, `getNRI`

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)
glmnri

plot(glmnri)
```

hsdardocs *Load additional documents*

Description

Access help documents and references for different methods.

Usage

```
hsdardocs(doc)
```

Arguments

doc	Name of document to load. Currently, only "References.pdf" and "Copyright" are available

Author(s)

Lukas Lehnert

Examples

```
## Not run:
## Open references of hyperspectral vegetation indices (PDF-file)
hsdardocs("References.pdf")

## See copyrights of routines and data used in hsdar-package (ascii-file)
hsdardocs("Copyright")

## End(Not run)
```

hsdar_parallel *hsdar_parallel*

Description

Get all functions which support parallel execution

Usage

```
hsdar_parallel()
```

Details

Parallel execution is performed via the **foreach**-package. Care is taken that a function will never run in parallel if the calling function is already using multicore processing.

Value

Vector containing supported function names

Author(s)

Lukas Lehnert

Examples

```
## Not run:
data(spectral_data)
## Load library
library(doMC)
## Register number of workers
registerDoMC(3)

supported_functions <- hsdar_parallel()
supported_functions

## Transform speclib using 3 cores
bd <- transformSpeclib(spectral_data)

## End(Not run)
```

HyperSpecRaster *Handle hyperspectral cubes using raster package*

Description

Methods to create and handle objects of class HyperSpecRaster

Usage

```
## S4 method for signature 'character,numeric'
HyperSpecRaster(x, wavelength, fwhm = NULL, attributes = NULL, ...)

## S4 method for signature 'RasterLayer,numeric'
HyperSpecRaster(x, wavelength, fwhm = NULL, attributes = NULL)

## S4 method for signature 'RasterBrick,numeric'
HyperSpecRaster(x, wavelength, fwhm = NULL, attributes = NULL)

## S4 method for signature 'HyperSpecRaster'
HyperSpecRaster(x, wavelength)

## S4 method for signature 'Speclib,ANY'
brick(x, nrow, ncol, xmn, xmx, ymn, ymx, crs)
```

```
## S4 method for signature 'Speclib,ANY'
HyperSpecRaster(x, nrow, ncol, xmn, xmx, ymn, ymx, crs)

## S4 method for signature 'HyperSpecRaster,character'
writeStart(x, filename, ...)

## S4 method for signature 'HyperSpecRaster'
getValuesBlock(x, ...)

## S4 method for signature 'RasterLayer,Speclib'
writeValues(x, v, start)

## S4 method for signature 'RasterBrick,Speclib'
writeValues(x, v, start)

## S4 method for signature 'HyperSpecRaster,Speclib'
writeValues(x, v, start)
```

Arguments

`x`	Raster* object
`wavelength`	Vector containing wavelength for each band
`fwhm`	Optional vector containing full-width-half-max values. If length == 1 the same value is assumed for each band. Note that function does not check the integrity of the values
`attributes`	Optional data.frame containing attributes data
`nrow`	Optional. Number of rows in HyperspecRaster. If omitted, function will try to get the information from the attributes in Speclib (`attr(x, "rastermeta")`)
`ncol`	Optional. Number of colums in HyperspecRaster. See nrow above.
`xmn`	Optional. Minimum coordiante in x-dimension. See nrow above.
`xmx`	Optional. Maximum coordiante in x-dimension. See nrow above.
`ymn`	Optional. Minimum coordiante in y-dimension. See nrow above.
`ymx`	Optional. Maximum coordiante in y-dimension. See nrow above.
`crs`	Optional. Object of class `'CRS'` giving the coordinate system for HyperspecRaster. See nrow above.
`...`	Additional arguments as for `brick`
`filename`	Name of file to create
`v`	Speclib or matrix of values
`start`	Integer. Row number (counting starts at 1) from where to start writing `v`

Value

HyperSpecRaster or RasterBrick

Author(s)

Lukas Lehnert

Examples

```
## Not run:
## Create raster file using PROSAIL
## Run PROSAIL
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.4, 0.1), 6)),
                        LAI = c(rep.int(0.5, 10), rep.int(1, 10),
                                rep.int(1.5, 10), rep.int(2, 10),
                                rep.int(2.5, 10), rep.int(3, 10)))
spectra <- PROSAIL(parameterList = parameter)

## Create SpatialPixelsDataFrame and fill data with spectra from PROSAIL
rows <- round(nspectra(spectra)/10, 0)
cols <- ceiling(nspectra(spectra)/rows)
grd <- SpatialGrid(GridTopology(cellcentre.offset = c(1,1,1),
                                cellsize = c(1,1,1),
                                cells.dim = c(cols, rows, 1)))
x <- SpatialPixelsDataFrame(grd, data = as.data.frame(spectra(spectra)))

## Write data to example file (example_in.tif) in workingdirectory
writeGDAL(x, fname = "example_in.tif", drivername = "GTiff")

## Examples for HyperSpecRaster using file example_in.tif
## Example 1:
## smoothing spectra
infile <- "example_in.tif"
outfile <- "example_result_1.tif"
wavelength <- spectra$wavelength

ra <- HyperSpecRaster(infile, wavelength)
tr <- blockSize(ra)

res <- writeStart(ra, outfile, overwrite = TRUE)
for (i in 1:tr$n)
{
  v <- getValuesBlock(ra, row=tr$row[i], nrows=tr$nrows[i])
  v <- smoothSpeclib(v, method="sgolay", n=25)
  res <- writeValues(res, v, tr$row[i])
}
res <- writeStop(res)

## Example 2:
## masking spectra and calculating vegetation indices
outfile <- "example_result_2.tif"
n_veg <- as.numeric(length(vegindex()))
res <- writeStart(ra, outfile, overwrite = TRUE, nl = n_veg)
for (i in 1:tr$n)
{
```

```
  v <- getValuesBlock(ra, row=tr$row[i], nrows=tr$nrows[i])
  mask(v) <- c(1350, 1450)
  v <- as.matrix(vegindex(v, index=vegindex()))
  res <- writeValues(res, v, tr$row[i])
}
res <- writeStop(res)

## End(Not run)
```

HyperSpecRaster-class *HyperSpecRaster* class*

Description

Extension of *RasterBrick-class to handle hyperspectral data

Details

Extension of *RasterBrick-class with three additional slots:

`wavelength`**:** A numeric vector giving the center wavelength for each band.

`fwhm` **(optional):** A numeric vector giving the full-width-half-max values for each band.

`attributes` **(optional):** A `data.frame` containing additional information for each pixel.

The information in the three slots are used for the convertion to `Speclib`.

Author(s)

Lukas Lehnert

See Also

`brick`, `Speclib`

---

idSpeclib *Handling IDs of spectra*

Description

Returning and setting ID of spectra in Speclib

Usage

```
idSpeclib(x)
idSpeclib(x) <- value
```

Arguments

`x`	Object of class `Speclib`.
`value`	Character vector of the same length as `nspectra(x)`, or NULL.

Value

For `idSpeclib<-`, the updated object. Otherwise a vector giving the ID of each spectrum in Speclib is returned.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

idSpeclib(spectral_data)
```

`import_USGS` *import USGS spectra*

Description

Import and download spectral data from USGS spectral library

Usage

```
USGS_get_available_files(url = NULL)

USGS_retrieve_files(avl = USGS_get_available_files(),
                    pattern = NULL, retrieve = TRUE,
                    loadAsSpeclib = TRUE, tol = 0.1)
```

Arguments

`url`	Character passing the url of the data. If NULL, the following URL is used: 'ftp://ftpext.cr.usgs.gov/pub/cr/co/denver/speclab/pub/spectral.library/splib06.library/ASCII/'
`avl`	List of available files. Typically the result of `USGS_get_available_files`.
`pattern`	Search pattern to define a subset of all available spectra.
`retrieve`	Logical. Should the data be downloaded?
`loadAsSpeclib`	Logical. If TRUE, an object of class "Speclib" is retured
`tol`	Discrepancy of the wavelength values between different spectra.

Author(s)

Lukas Lehnert

Examples

```
## Not run:
## Retrieve all available spectra
avl <- USGS_get_available_files()

## Download all spectra matching "grass-fescue"
grass_spectra <- USGS_retrieve_files(avl = avl, pattern = "grass-fescue")

plot(grass_spectra)

## End(Not run)
```

---

makehull *Check continuum line*

Description

Check if continuum line is intersecting the reflectance curve.

Usage

```
makehull(x, ispec)
```

Arguments

x	Object of class `Clman`.
ispec	Name or index of spectrum to be checked.

Value

Object of class `list`.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `addcp`, `deletecp`, `makehull`, `updatecl`

`Clman`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

## Add fix point at 4596 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2496)

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

hull <- makehull(spec_clman, 1)

## Transform spectra using band depth
spec_bd <- transformSpeclib(spec, method = "sh", out = "bd")

## Update continuum line of first spectrum
spec_bd <- updatecl(spec_bd, hull)

## Plot modified transformed spectrum
plot(spec_bd, FUN = 1)
```

`mask` *Mask spectra*

Description

Returning and setting mask of spectra in Speclib. `interpolate.mask` linearly interpolates masked parts in spectra.

Usage

```
## S4 method for signature 'Speclib'
mask(object)
## S4 replacement method for signature 'Speclib,data.frame'
mask(object) <- value
## S4 replacement method for signature 'Speclib,list'
mask(object) <- value
## S4 replacement method for signature 'Speclib,numeric'
mask(object) <- value

## Linear interpolation of masked parts
interpolate.mask(object)
```

Arguments

`object`	Object of class `Speclib`.
`value`	Numeric vector, data frame or list giving the mask boundaries in wavelength units. See details section.

Details

Value may be an object of class vector, data frame or list. Data frames must contain 2 columns with the first column giving the lower and the second the upper boundary values of the mask. List must have two items consisting of vectors of length = 2. The first entry is used as lower and the second as upper boundary values. Vectors must contain corresponding lower and upper boundary values consecutively.

Interpolation of masked parts is mainly intended for internal use. Interpolation is only possible if mask does not exceed spectral range of Speclib.

Value

For `mask<-`, the updated object. Otherwise a data frame giving the mask boundaries.

`interpolate.mask` returns a new object of class Speclib.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`Speclib`

Examples

```
data(spectral_data)

mask(spectral_data) ## NULL
```

```
## Mask from vector
spectral_data_ve <- spectral_data
mask(spectral_data_ve) <- c(1040,1060,1300,1450)
mask(spectral_data_ve)


## Mask from data frame
spectral_data_df <- spectral_data
mask(spectral_data_df) <- data.frame(lb=c(1040,1300),ub=c(1060,1450))
mask(spectral_data_df)


## Mask from list
spectral_data_li <- spectral_data
mask(spectral_data_li) <- list(lb=c(1040,1300),ub=c(1060,1450))
mask(spectral_data_li)

## Linear interpolation
plot(spectral_data)
plot(interpolate.mask(spectral_data_li), new=FALSE)
```

`meanfilter` *Apply mean filter*

Description

Apply mean filter to data frame with spectra as rows and bands as columns. Filter size is passed as number of bands averaged at both sites of the respective band value.

Usage

```
meanfilter(spectra, p = 5)
```

Arguments

`spectra`	Data frame containing spectra
`p`	Filter size.

Value

Filtered data frame of same dimension as input data frame

Author(s)

Lukas Lehnert

See Also

`smoothSpeclib`

Examples

```
data(spectral_data)

spectra_filtered <- meanfilter(spectra(spectral_data), p = 10)
spectra(spectral_data) <- spectra_filtered
```

---

merge *Merge speclibs*

Description

Merge 2 Speclibs and their attributes data

Usage

```
## S4 method for signature 'Speclib,Speclib'
merge(x, y, ...)
```

Arguments

x	1st Object of class Speclib to be merged.
y	2nd Object of class Speclib to be merged.
...	Further arguments passed to generic functions. Currently ignored.

Value

Object of class Speclib.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)
sp1 <- spectral_data[c(1:10),]
sp2 <- spectral_data[c(11:20),]

speclib_merged <- merge(sp1, sp2)
```

nri — *Normalised ratio index*

Description

Calculate normalised ratio index for a single given band combination or for all possible band combinations

Usage

```
nri(x, b1, b2, recursive = FALSE, bywavelength = TRUE)
```

Arguments

`x`	List of class `Speclib` or of class `Nri` for print and as.matrix methods
`b1`	Band 1 given as index or wavelength
`b2`	Band 2 given as index or wavelength
`recursive`	If TRUE indices for all possible band combinations are calculated
`bywavelength`	Flag to determine if b1 and b2 are indices (bywavelength = FALSE) or wavelength (bywavelength = TRUE)
`...`	Further arguments passed to generic functions. Currently ignored.

Details

Function performs the following calculation:

$$nri_{B1,\ B2} = \frac{R_{B1} - R_{B2}}{R_{B1} - R_{B2}};$$

with R being reflectance values at wavelength $B1$ and $B2$, respectively.

If recursive = TRUE, all possible band combinations are calculated.

Value

If recursive = FALSE, a data frame with index values is returned. Otherwise result is an object of class `nri`. See `glm.nri` for applying a generalised linear model to an array of normalised ratio indices.

Author(s)

Lukas Lehnert

References

Sims, D.A.; Gamon, J.A. (2002). Relationships between leaf pigment content and spectral reflectance across a wide range of species, leaf structures and developmental stages. Remote Sensing of Environment: 81/2, 337 - 354.

Thenkabail, P.S.; Smith, R.B.; Pauw, E.D. (2000). Hyperspectral vegetation indices and their relationships with agricultural crop characteristics. Remote Sensing of Environment: 71/2, 158 - 182.

See Also

glm.nri, glm, Speclib, Nri

Examples

```
data(spectral_data)

## Calculate NDVI
ndvi <- nri(spectral_data, b1=800, b2=680)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)
nri_WV
```

Nri-class   * *Nri class*

Description

Class to handle datasets containing normalized ratio indices of spectra.

Details

Object with slots:

- nri: Object of class DistMat3D containing nri values.
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- wavelength: Vector with wavelength information.
- dimnames: Character vector containing band names used to calculate nri-values.
- multivariate: List defining the kind of test/model applied to the data and the model data. Only used after object has passed e.g. (g)lm.nri.
- attributes: Data.frame containing additional data
- usagehistory: Vector giving information on history of usage of the object.

Note

See figure in hsdar-package for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

Speclib

Nri-methods   *Methods for * Nri-class*

Description

Methods to handle data in objects of class Nri.

Usage

```
## S4 method for signature 'Nri'
as.matrix(x, ..., named_matrix = TRUE)

## S4 method for signature 'Nri'
as.data.frame(x, na.rm = FALSE, ...)

## S4 method for signature 'Nri'
wavelength(object)

getFiniteNri(x)
```

Arguments

x,object	List of class 'Nri'
na.rm	Remove indices containing NA-values. Note that if TRUE, all indices are removed which have at least one NA value.
named_matrix	Flag if column and row names are set to band indices used for the calculation of the nri-values.
...	Further arguments passed to generic functions. Currently ignored.

Author(s)

Lukas Lehnert

See Also

glm.nri, glm

nri_best_performance *Best performing model(s) with NRI*

Description

Get or mark best performing model(s) between narrow band indices and environmental variables

Usage

```
nri_best_performance(nri, n = 1, coefficient = "p.value",
                     predictor = 2, abs = FALSE, findMax = FALSE,
                     ...)
mark_nri_best_performance(best, glmnri, n = nrow(best$Indices),
                          uppertriang = FALSE, ...)
```

Arguments

`nri`	Object of class nri
`glmnri`	Object of class glmnri
`n`	Number of models to return or mark
`coefficient`	Name or index of coefficient to plot
`predictor`	Name or index of term to plot
`abs`	Use absolute value (e.g. for t-values)
`findMax`	Find maximum or minimum values
`best`	Output from `nri_best_performance`
`uppertriang`	Flag to mark the upper triangle
`...`	Further arguments passed to `glm` function. These must be the same as used for initial creation of `glm.nri`. For `mark_nri_best_performance` arguments are passed to `polygon`.

Details

See details in `glm.nri` and `glm`.

Author(s)

Lukas Lehnert

See Also

`glm.nri`, `glm`

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Build glm-models
glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Return best 5 models
BM <- nri_best_performance(glmnri, n = 5, coefficient = "p.value")

## Get nri values for the 5 models
nri_BM <- getNRI(nri_WV, BM)
```

---

plot.Nri — *Plot function for (g)lm.nri and cor.test.nri*

Description

Plot values in (generalised) linear modes and correlation tests from narrow band indices

Usage

```
## S4 method for signature 'Nri'
plot(x, coefficient = "p.value", predictor = 2,
     xlab = "Wavelength band 1 (nm)",
     ylab = "Wavelength band 2 (nm)", legend = TRUE,
     colspace = "hcl", col = c(10, 90, 60, 60, 10, 80),
     digits = 2, range = "auto", constraint  = NULL,
     uppertriang = FALSE, ...)
```

Arguments

`x`	Object to be plotted.
`coefficient`	Name or index of coefficient to plot.
`predictor`	Name or index of term to plot.
`xlab`	Label for x-axis.
`ylab`	Label for y-axis.
`legend`	Flag if legend is plotted. If `legend == "outer"` the legend is plotted in the outer margins of the figure. This is useful if both diagonals are used.
`colspace`	Either "hcl" or "rgb". Colour space to be used for the plots.

col	If colspace == "hcl", the vector is giving the minimum and maximum values of hue (element 1 & 2), chroma (element 3 & 4) and luminance (element 5 & 6). The optional element 7 is used as alpha value. See hcl for further explanation. If colspace == "rgb", a vector of length >=2 giving the colours to be interpolated using colorRamp.
digits	Precision of labels in legend.
range	"auto" or a vector of length = 2 giving the range of values to be plotted.
constraint	A character string giving a constraint which values should be plotted. See examples section.
uppertriang	Flag if upper triangle is used for the plot. Note that if TRUE the current plot is used instead of starting a new plot
...	Further arguments passed to plot.default.

Details

See details in glm.nri and glm.

Value

An invisible vector with minimum and maximum values plotted.

Author(s)

Lukas Lehnert

See Also

nri, glm.nri, glm, cor.test, t.test

Examples

```
## Not run:
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Fit generalised linear models between NRI-values and chlorophyll
glmnri <- glm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Plot p-values
plot(glmnri, range = c(0, 0.05))
## Plot t-values
plot(glmnri, coefficient = "t.value")
## Plot only t-values where p-values < 0.001
plot(glmnri, coefficient = "t.value",
     constraint = "p.value < 0.001")
```

```
## Fit linear models between NRI-values and chlorophyll
lmnri <- lm.nri(nri_WV ~ chlorophyll, preddata = spec_WV)

## Plot r.squared
plot(lmnri)

## Example for EnMAP (Attention: Calculation time may be long!)
spec_EM <- spectralResampling(spectral_data, "EnMAP",
                              response_function = FALSE)
mask(spec_EM) <- c(300, 550, 800, 2500)
nri_EM <- nri(spec_EM, recursive = TRUE)
glmnri <- glm.nri(nri_EM ~ chlorophyll, preddata = spec_EM)

## Plot T values in lower and p-values in upper diagonal
## of the plot
## Enlarge margins for legends
par(mar = c(5.1, 4.1, 4.1, 5))
plot(glmnri, coefficient = "t.value", legend = "outer")
plot(glmnri, coefficient = "p.value", uppertriang = TRUE)
lines(c(400,1705),c(400,1705))

## End(Not run)
```

`plot.Specfeat` *Plot function for class Specfeat*

Description

Plot spectra in Specfeat objects

Usage

```
## S4 method for signature 'Specfeat,ANY'
plot(x, fnumber = 1, stylebysubset = NULL, changecol = TRUE,
        changetype = FALSE, autolegend = TRUE, new = TRUE, ...)
```

Arguments

`x`	Object to be plotted
`fnumber`	Subscript of feature(s) to be plotted
`stylebysubset`	Name of column in attributes to be used for colour.
`changecol`	Flag indicating if line colours change according to values in coloumn defined by stylebysubset
`changetype`	Flag indicating if line types change according to values in coloumn defined by stylebysubset
`autolegend`	Flag if legend is plotted.
`new`	Flag if a new plot is started.
`...`	Further arguments passed to `plot.default`

Author(s)

Lukas Lehnert

See Also

nri, glm.nri, glm, cor.test,Nri-method, t.test,Nri-method

Examples

```
## See examples in specfeat
```

---

plot.Speclib *Plot speclib*

Description

Plot Speclib in a new plot or adding it to an existing plot.

Usage

```
## S4 method for signature 'Speclib,ANY'
plot(x, FUN = NULL, new = TRUE, ...)

## S4 method for signature 'Clman,ANY'
plot(x, ispec, subset = NULL, numeratepoints = TRUE,
    hull.style = NULL, points.style = list(), ...)
```

Arguments

x	Object of class Speclib.
FUN	Name of a function (character) or index or ID of single spectrum to plot (integer).
new	If FALSE the plot is added to active existing plot.
ispec	Subscript of spectrum to be plotted.
subset	Vector of length = 2 containing minimum and maximum wavelength to plot.
numeratepoints	Flag if continuum points are numerated and labeled.
hull.style	List of arguments passed to lines to construct the continuum line.
points.style	List of arguments passed to points to construct the continuum points. May be NULL to suppress plotting of fix points.
...	Further arguments passed to internal plot functions or to plot for objects of class Speclib and Clman.

Details

The function may work in a couple of modes. The default way is to plot mean values (solid line) of all spectra and the standard deviations within bands. If data is assumed to be continuous the standard deviations are plotted as dashed lines otherwise error bars will indicate standard deviations.

The user has various options to change the way things are looking: With argument `FUN` the name of a function, the ID or the index of a certain spectrum may be specified. Note that if `FUN` is a function, this function will be applied to all spectra. If function should be applied to a subset of spectra, use function `subset` to define rules excluding certain spectra.

By passing a subset, the user may specify a spectral range to plot. Limits for x- and y-axis will be found automatically or may be passed separately.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

## Set mask for channel crossing and water absorption bands
mask(spectral_data) <- c(1040, 1060, 1350, 1450)

## Simple example
plot(spectral_data, legend = list(x = "topleft"))

## Example with groups
plot(spectral_data, bygroups = TRUE, legend = list(x = "topleft"))

## Example with function
par(mfrow = c(2,3))
plot(spectral_data, FUN = "min", main = "Minimum of speclib")
plot(spectral_data, FUN = "max", main = "Maximum of speclib")
plot(spectral_data, FUN = "median", main = "Median of speclib")
plot(spectral_data, FUN = "mean", main = "Mean of speclib")
plot(spectral_data, FUN = "var", main = "Variance of speclib")
```

`PROSAIL` *Simulate canopy spectrum*

Description

Simulate a canopy spectrum using PROSAIL 5B

Usage

```
PROSAIL(N = 1.5, Cab = 40, Car = 8, Cbrown = 0.0,
        Cw = 0.01, Cm = 0.009, psoil = 0, LAI = 1,
        TypeLidf = 1, lidfa = -0.35, lidfb = -0.15,
        hspot = 0.01, tts = 30, tto = 10, psi = 0,
        parameterList = NULL, rsoil = NULL)
```

Arguments

`N`	Structure parameter
`Cab`	Chlorophyll content
`Car`	Carotenoid content
`Cbrown`	Brown pigment content
`Cw`	Equivalent water thickness
`Cm`	Dry matter content
`psoil`	Dry/Wet soil factor
`LAI`	Leaf area index
`TypeLidf`	Type of leaf angle distribution. See details section
`lidfa`	Leaf angle distribution. See details section
`lidfb`	Leaf angle distribution. See details section
`hspot`	Hotspot parameter
`tts`	Solar zenith angle
`tto`	Observer zenith angle
`psi`	Relative azimuth angle
`parameterList`	An optional object of class `'data.frame'`. Function will iterate over rows of parameterList setting missing entries to default values. See examples section.
`rsoil`	An optional object of class `'Speclib'` containing the background (soil) reflectance. Note that reflectance values must be in range [0...1].

Details

This function uses the FORTRAN code of PROSAIL model (Version 5B). For a general introduction see following web page and the links to articles provided there:

http://teledetection.ipgp.jussieu.fr/prosail/

The following table summarises the abbreviations of parameters and gives their units as used in PROSAIL. Please note that default values of all parameters were included with the intention to provide an easy access to the model and should be used with care in any scientific approach!

Parameter	Description of parameter	Units
N	Leaf structure parameter	NA
Cab	Chlorophyll a+b concentration	μg/cm^2

Car	Carotenoid concentration	μg/cm^2
Caw	Equivalent water thickness	cm
Cbrown	Brown pigment	NA
Cm	Dry matter content	g/cm^2
LAI	Leaf Area Index	NA
psoil	Dry/Wet soil factor	NA
hspot	Hotspot parameter	NA
tts	Solar zenith angle	deg
tto	Observer zenith angle	deg
psi	Relative azimuth angle	deg

Functions for distribution of leaf angles within the canopy may work in two modes, which is controlled via `TypeLidf`:

1. `TypeLidf == 1` (default): `lidfa` is the average leaf slope and `lidfb` describes bimodality of leaf distribution. The following list gives an overview on typical settings:

LIDF type	`lidfa`	`lidfb`
Planophile	1	0
Erectophile	-1	0
Plagiophile	0	-1
Extremophile	0	1
Spherical (default)	-0.35	-0.15

2. `TypeLidf != 1`: `lidfa` is the average leaf angle in degree (0 = planophile / 90 = erectophile); `lidfb` is 0

Value

An object of class `Speclib`. If parameterList is used, the parameter are stored in attributes table of `Speclib`.

Note

The function is based on the FORTRAN version of the PROSAIL-code initially developed by Stephane JACQUEMOUD, Jean-Baptiste FERET, Christophe FRANCOIS and Eben BROADBENT. SAIL component has been developed by Wout VERHOEF.

Author(s)

Lukas Lehnert

References

Jacquemoud, S., Verhoef, W., Baret, F., Bacour, C., Zarco-Tejada, P.J., Asner, G.P., Francois, C., and Ustin, S.L. (2009): PROSPECT + SAIL models: a review of use for vegetation characterization, Remote Sensing of Environment, 113, S56-S66.

See Also

PROSPECT, Speclib

Examples

```
## Single spectrum
spectrum <- PROSAIL(N = 1.3)
plot(spectrum)

## Example using parameterList
## Test effect of leaf structure and LAI on spectra
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.5, 0.5), 2)),
                        LAI = c(rep.int(0.5, 3), rep.int(1, 3)))
spectra <- PROSAIL(parameterList = parameter)

## Print attributes table
attribute(spectra)

## Plot spectra
plot(subset(spectra, LAI == 0.5), col = "red", ylim = c(0, 0.3))
plot(subset(spectra, LAI == 1), col = "green", new = FALSE)
```

PROSPECT — *Simulate plant spectrum*

Description

Simulate plant spectrum using PROSPECT 5. The inversion uses the concept after Feret et al. (2008).

Usage

```
PROSPECT(N = 1.5, Cab = 40, Car = 8, Cbrown = 0.0,
         Cw = 0.01, Cm = 0.009, transmittance = FALSE,
         parameterList = NULL)
## Inversion
PROSPECTinvert(x, P0 = NULL, transmittance_spectra = NULL,
               sam = FALSE, ...)
```

Arguments

`N`	Structure parameter
`Cab`	Chlorophyll content
`Car`	Carotenoid content
`Cbrown`	Brown pigment content
`Cw`	Equivalent water thickness
`Cm`	Dry matter content

`transmittance` Logical flag, if transmittance instead of reflectance values are returned.

`parameterList` An optional object of class `'data.frame'`. Function will iterate over rows of parameterList setting missing entries to default values. See examples section.

`x, transmittance_spectra` Speclib(s) containing the reflectance/transmittance values to be simulated during inversion of PROSPECT.

`P0` Initial set of parameters (N, Cab etc.).

`sam` Logical if spectral angle mapper is used as distance measurement. If FALSE, the root mean square error is used. Note that this flag has only an effect if no transmittance spectra are passed.

`...` Parameters passed to `nelder_mead` from the **pracma**-package

Details

This function uses the FORTRAN code of PROSPECT model (Version 5). For a general introduction see following web page and the links to articles provided there:

http://teledetection.ipgp.jussieu.fr/prosail/

The following table summarises the abbreviations of parameters and gives their units as used in PROSPECT. Please note that default values of all parameters were included with the intention to provide an easy access to the model and should be used with care in any scientific approach!

Parameter	Description of parameter	Units
N	Leaf structure parameter	NA
Cab	Chlorophyll a+b concentration	$\mu g/cm^2$
Car	Carotenoid concentration	$\mu g/cm^2$
Cw	Equivalent water thickness	cm
Cbrown	Brown pigment	NA
Cm	Dry matter content	g/cm^2

The inversion uses the function `nelder_mead` from the **pracma**-package and implements the Matlab-Code developed by Feret et al. (2008).

Value

An object of class `Speclib`.

Note

The function is based on the FORTRAN version of the PROSPECT-code initially developed by Jean-Baptiste FERET, Stephane JACQUEMOUD and Christophe FRANCOIS.

Author(s)

Lukas Lehnert

References

Jacquemoud, S. and Baret, F. (1990). PROSPECT: A model of leaf optical properties spectra, Remote Sensing of Environment 34: 75 - 91.

Feret J.B., Francois C., Asner G.P., Gitelson A.A., Martin R.E., Bidel L.P.R., Ustin S.L., le Maire G., & Jacquemoud S. (2008), PROSPECT-4 and 5: advances in the leaf optical properties model separating photosynthetic pigments. Remote Sensing of Environment, 112, 3030-3043.

See Also

PROSAIL, nelder_mead, Speclib

Examples

```
## Single spectrum
spectrum <- PROSPECT(N = 1.3, Cab = 30, Car = 10, Cbrown = 0,
                     Cw = 0.01, Cm = 0.01)
plot(spectrum)

## Example using parameterList
## Test effect of leaf structure and chlorophyll content on
## spectra
parameter <- data.frame(N = c(rep.int(seq(0.5, 1.5, 0.5), 2)),
                        Cab = c(rep.int(40, 3), rep.int(20, 3)))
spectra <- PROSPECT(parameterList = parameter)

## Print attributes table
attribute(spectra)

## Plot spectra for range from 400 to 800 nm
spectra <- spectra[,wavelength(spectra) >= 400 &
                    wavelength(spectra) <= 800]

plot(subset(spectra, Cab == 20), col = "red", ylim = c(0, 0.5))
plot(subset(spectra, Cab == 40), col = "green", new = FALSE)
```

Raster-methods   *Rasterbased methods for spectra*

Description

Methods to manipulate and save spectra in Speclibs stored as RasterBrick

Usage

```
## S4 method for signature 'Speclib,ANY'
extract(x, y, ...)

## S4 method for signature 'Speclib,character'
writeRaster(x, filename, ...)
```

Arguments

`x`	Speclib with RasterBrick-object for spectra
`y`	Object of any valid type to define area to extract
`filename`	Output filename
`...`	Additionaly arguments passed to basic funtions in the raster-package

Value

Speclib

Author(s)

Lukas Lehnert

`rastermeta` *Create list containing rastermeta-information*

Description

Create valid objects for slot `rastermeta` in `Speclib`.

Usage

```
rastermeta(x, dim, ext, crs)
```

Arguments

`x`	Optional. Object of one of the following classes: "Raster", "RasterBrick", "RasterStack", "HyperSpecRaster".
`dim`	Optional. Vector with length == 2. The first and second elements give the number of rows and columns, respectively.
`ext`	Optional. Object of class `extent`.
`crs`	Optional. Object of class `CRS`.

Value

List with following elements (in exactly this order!):

- dim: Vector with length == 2. The first and second elements give the number of rows and columns, respectively.
- ext: Object of class `extent`.
- crs: Object of class `CRS`.

Author(s)

Lukas Lehnert

See Also

Speclib, HyperSpecRaster

---

rededge *Red edge parameter*

Description

Derive red edge parameters from hyperspectral data

Usage

```
rededge(x, smooth = TRUE, round = FALSE, ...)
```

Arguments

x	List of class Speclib
smooth	Logical indicating if spectral data should be smoothed. See details section.
round	Logical indicating if resulting wavelength position should be rounded.
...	Further arguments passed to derivative.speclib

Details

Shape and location of the red edge are commonly described by four parameters:

- $R0$: minimum reflectance in the red spectrum
- $\lambda 0$: wavelength of the minimum reflectance
- λp: inflection point
- Rs: shoulder wavelength

The red edge parameters are calculated as proposed in Bach (1995) from the spectral area between 550 and 900 nm. $\lambda 0$ is calculated as the last root before the maximum value of the 2nd derivation. The minimum reflectance is the reflectance at ($\lambda 0$). The inflection point is the root of the 2nd derivative function between the maximum value and the minimum value. The shoulder wavelength is the first root beyond the minimum value of the 2nd derivation.

Optional smoothing is performed with

```
smoothSpeclib(x, method = "spline", n = round(nbands(x)/10,0))
```

prior to all calculations. Note that reflectance values returned by the `rededge`-function are original values and not the smoothed reflectances. This would not be the case, if already smoothed reflectance values are passed to `rededge`-function.

Value

A data frame containing parameters for each spectrum.

Author(s)

Hanna Meyer

References

Bach, H. (1995): Die Bestimmung hydrologischer und landwirtschaftlicher Oberflaechenparameter aus hyperspektralen Fernerkundungsdaten. Muenchner Geographische Abhandlungen Reihe B, Band B21.

See Also

vegindex, derivative.speclib, smoothSpeclib

Examples

```
data(spectral_data)
rd <- rededge(spectral_data)
boxplot(rd$R0 ~ attribute(spectral_data)$season, ylab = "R0")
```

---

response_functions   *Satellite sensor response functions*

Description

Satellite sensor response functions for all sensor channels

Format

An object of class 'data.frame'

Details

Please do not access this data directly, since it contains only the response values without any spectral information. To get response functions use function get.response, instead.

Note

This data is kindly provided by operators of satellites. See hsdardocs("Copyright") for copyright information on spectral response functions.

- Quickbird: Copyright by DigitalGlobe, Inc. All Rights Reserved
- RapidEye: Copyright by RapidEye AG
- WorldView-2: Copyright by DigitalGlobe, Inc. All Rights Reserved

smgm *SMGM*

Description

Calculate Gaussian model on soil spectra

Usage

```
smgm(x, percentage = TRUE, gridsize = 50)
```

Arguments

`x`	Object of class Speclib.
`percentage`	Flag if spectra in x are in range [0, 100]. If FALSE, the spectra are scaled to [0,100].
`gridsize`	Size of the grid used to perform least squares approximation.

Details

The algorithm fits a Gaussian function to the continuum points of the spectra in the spectral region between approx. 1500 to 2500 nm. The continuum points are derived constructing the convex hull of the spectra (see `transformSpeclib`). The Gaussian function requires three parameter: (1) the mean values which is set to the water fundamental of 2800 nm, (2) the absorption depth at 2800 nm, and (3) the distance to the inflection point of the function. The latter two parameters are iteratively chosen using a grid search. The mesh size of the grid can be adjusted with the `gridsize` parameter. Note that the function requires the spectral reflectance values to be in interval [0, 100].

Value

Object of class `Speclib` containing the fitted Gaussian spectra and the parameters derived from the Gaussian curve. The three parameters (absorption depth, R0; distance to the inflection point, sigma; area between the curve and 100 % reflectance, area) are stored in the attributes of the new Speclib. Additionally, the function returns the final root mean square error of the Gaussian fit.

Note

The code is based on the IDL functions written by Michael L. Whiting.

Author(s)

Lukas Lehnert

References

Whiting, M. L., Li, L. and Ustin, S. L. (2004): Predicting water content using Gaussian model on soil spectra. Remote Sensing of Environment, 89, 535-552.

See Also

soilindex, Speclib

Examples

```
## Use PROSAIL to simulate spectra with different soil moisture content
Spektr.lib <- smoothSpeclib(PROSAIL(parameterList = data.frame(psoil = seq(0,1,0.1), LAI = 0)))

smgm_val <- smgm(Spektr.lib)

for (i in 1:nspectra(smgm_val))
  plot(smgm_val, FUN = i, new = i==1, col = i)

attribute(smgm_val)
```

---

smoothSpeclib — *Smooth spectra*

Description

Smooth spectra using Savitzky-Golay filtering, lowess-, spline-functions or mean filter.

Usage

```
smoothSpeclib(x, method = "mean", ...)
```

Arguments

x	Object of class Speclib.
method	Character string giving the method to be used. Predefined valid options are "sgolay", "lowess", "spline" and "mean". However, method can also be the (character) name of any other filter function (see examples).
...	Further arguments passed to filter functions. See examples.

Details

This function allows filtering using four different methods:

- Savitzky-Golay: Smoothing applying Savitzky-Golay-Filter. See sgolayfilt for details.
- Lowess: Smoothing applying lowess-Filter. See lowess for details.
- Spline: Smoothing applying spline-Filter. See spline for details.
- Mean: Smoothing applying mean-Filter. See meanfilter for details.

Value

Object of class Speclib.

Author(s)

Lukas Lehnert

References

Tsai, F. & Philpot, W. (1998): Derivative analysis of hyperspectral data. Remote Sensing of Environment 66/1. 41-51.

See Also

sgolayfilt, lowess, spline, meanfilter

Examples

```
data(spectral_data)

## Example of predefined filter functions
## Savitzky-Golay
sgolay <- smoothSpeclib(spectral_data, method="sgolay", n=25)

## Spline
spline <- smoothSpeclib(spectral_data, method="spline",
                        n=round(nbands(spectral_data)/10,0))

## Lowess
lowess <- smoothSpeclib(spectral_data, method="lowess", f=.01)

## Mean
meanflt <- smoothSpeclib(spectral_data, method="mean", p=5)

par(mfrow=c(2,2))
plot(spectral_data, FUN=1, main="Savitzky-Golay")
plot(sgolay, FUN=1, new=FALSE, col="red", lty="dotted")
plot(spectral_data, FUN=1, main="Spline")
plot(spline, FUN=1, new=FALSE, col="red", lty="dotted")
plot(spectral_data, FUN=1, main="Lowess")
plot(lowess, FUN=1, new=FALSE, col="red", lty="dotted")
plot(spectral_data, FUN=1, main="Mean")
plot(meanflt, FUN=1, new=FALSE, col="red", lty="dotted")

## Example of a not predefined filter function (Butterworth filter)
bf <- butter(3, 0.1)
bf_spec <- smoothSpeclib(spectral_data, method="filter", filt=bf)
plot(spectral_data, FUN=1, main="Butterworth filter")
plot(bf_spec, FUN=1, new=FALSE, col="red", lty="dotted")
```

`soilindex` *soilindex*

Description

Function calculates a variety of hyperspectral soil indices

Usage

```
soilindex(x, index, returnHCR = "auto", weighted = TRUE, ...)
```

Arguments

`x`	Object of class `Speclib`
`index`	Character string. Name or definition of index or vector with names/definitions of indices to calculate. See Details section for further information.
`returnHCR`	If TRUE, the result will be of class HyperSpecRaster, otherwise it is a data frame. If "auto", the class is automatically determined by passed Speclib.
`weighted`	Logical indicating if reflectance values should be interpolated to fit wavelength position. If `FALSE` the reflectance values of nearest neighbour to passed position are returned. See `get_reflectance` for further explanation.
`...`	Further arguments passed to derivative functions. Only used for indices requiring derivations.

Details

Index must be a charater vector containing pre-defined indices (selected by their name) or self defined indices or any combination of pre- and self-defined indices.

Pre-defined indices: The following indices are available:

Name	**Formula**	**Reference***
BI_TM	$((TM\_1^2 + TM\_2^2 + TM\_3^2)/3)^{0.5}$**	Mathieu et al. (1998)
CI_TM	$(TM\_3 - TM\_2)/(TM\_3 + TM\_2)$**	Escadafal and Huete (1991)
HI_TM	$(2 \cdot TM\_3 - TM\_2 - TM\_1)/(TM\_2 - TM\_1)$**	Escadafal et al. (1994)
NDI	$(R_{840} - R_{1650})/(R_{840} + R_{1650})$	McNairn, H. and Protz, R. (1993)
NSMI	$(R_{1800} - R_{2119})/(R_{1800} + R_{2119})$	Haubrock et al. (2008)
RI	$R_{693}^2/(R_{447} \cdot R_{556}^3)$	Ben-Dor et al. (2006)
RI_TM	$TM\_3^2/(TM\_1 \cdot TM\_2^3)$**	Madeira et al. (1997), Mathieu et al. (1998)
SI_TM	$(TM\_3 - TM\_1)/(TM\_3 + TM\_1)$**	Escadafal et al. (1994)
SWIR SI	$-41.59 \cdot (R_{2210} - R_{2090}) + 1.24 \cdot (R_{2280} - R_{2090}) + 0.64$	Lobell et al. (2001)

* For references please type: `hsdardocs("References.pdf")`.
** TM_1 denotes the first band of Landsat Thematic Mapper. Consequently, the hyperspectral data is resmapled to Landsat TM using `spectralResampling` prior to the calculation of the index. For resampling, the spectral response function is used.

Self-defining indices:

Self-defined indices may be passed using the following syntax:

- Rxxx: Reflectance at wavelength 'xxx'. Note that R must be upper case.
- Dxxx: First derivation of reflectance values at wavelength 'xxx'. Note that D must be upper case.

Using this syntax, complex indices can be easily defined. Note that the entire definition of the index must be passed as one character string. Consequently, the NSMI would be written as "(R1800-R2119)/(R1800+R2119)".

Value

A vector containing indices values. If index is a vector with length > 1, a data frame with ncol = length(index) and nrow = number of spectra in x is returned.

If function is called without any arguments, return value will be a vector containing all available indices in alphabetical order.

Author(s)

Lukas Lehnert

References

See `hsdardocs("References.pdf")`

See Also

`vegindex`, `get_reflectance`

Examples

```
data(spectral_data)
## Example calculating all available indices
## Get available indices

avl <- soilindex()
vi <- soilindex(spectral_data, avl)
```

specfeat *Function to isolate spectral features*

Description

Function isolates specified absorption features previously identified by define.features.

Usage

```
specfeat(x, FWL)

## S4 method for signature 'Specfeat'
plot(x, fnumber = 1, stylebysubset = NULL, changecol = TRUE,
     changetype = FALSE, autolegend = TRUE, new = TRUE, ...)
```

Arguments

x	Object of class Speclib containing the band depth or ratio transformed reflectance spectra with additional information on feature limits calculated by define.features. For plot this must be object of class specfeat.
FWL	A vector containing one wavelength per feature to be isolated, e.g. the major absorption features. Features which include these specified wavelengths will be isolated.
fnumber	Index of feature(s) to be plotted.
stylebysubset	Name of variable to be used as grouping factor. May be selected from attributes table, groups or subgroups and must be convertible to factors.
changecol	Flag, if line colour should be varied among groups
changetype	Flag, if line styles should be varied among groups
autolegend	Flag if, legend is printed automatically.
new	Create new plot or add data to existing one.
...	Further arguments passed to plot function.

Value

An object of class Specfeat containing the isolated features.

Author(s)

Hanna Meyer and Lukas Lehnert

See Also

define.features, cut_specfeat, Specfeat

Examples

```
data(spectral_data)

## Transform speclib
bd <- transformSpeclib(spectral_data, method = "sh", out = "bd")

## Define features automatically
features <- define.features(bd)

##Example to isolate the features around 450nm, 700nm, 1200nm and 1500nm.
featureSelection <- specfeat(features, c(450,700,1200,1500))

## Plot features
plot(featureSelection, 1:4)

## Advanced plotting example
plot(featureSelection, 1:4, stylebysubset = "season")

plot(featureSelection, 1:4, stylebysubset = "season", changecol = FALSE,
     changetype = TRUE)
```

`Specfeat-class` ** Specfeat class*

Description

Class to handle spectral feature data.

Details

Class extends `Speclib`-class and adds two additional slots:

- features: List containing the spectra according to the features.
- featureLimits: List containing limits of features defined by `define.features`.

Note

See figure in `hsdar-package` for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

`Speclib`

speclib *Methods to create objects of class Speclib*

Description

Methods to create objects of class Speclib from various data types

Usage

```
## S4 method for signature 'matrix,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'SpatialGridDataFrame,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'numeric,numeric'
speclib(spectra, wavelength, ...)

## S4 method for signature 'matrix,data.frame'
speclib(spectra, wavelength, ...)

## S4 method for signature 'SpatialGridDataFrame,data.frame'
speclib(spectra, wavelength, ...)

## S4 method for signature 'numeric,data.frame'
speclib(spectra, wavelength, ...)

## S4 method for signature 'matrix,matrix'
speclib(spectra, wavelength, ...)

## S4 method for signature 'SpatialGridDataFrame,matrix'
speclib(spectra, wavelength, ...)

## S4 method for signature 'numeric,matrix'
speclib(spectra, wavelength, ...)

## S4 method for signature 'HyperSpecRaster,ANY'
speclib(spectra, wavelength, ...)

## S4 method for signature 'Speclib'
print(x)

## S4 method for signature 'Speclib'
show(object)

createspeclib(spectra, wavelength, fwhm = NULL, attributes = NULL,
        usagehistory = NULL, transformation = NULL,
```

```
continuousdata = "auto", wlunit = "nm",
          xlabel = "Wavelength", ylabel = "Reflectance",
          rastermeta = NULL)

is.speclib(x)
```

Arguments

`spectra`	Data frame, matrix of raster object of class 'RasterBrick' or 'SpatialGridDataFrame' with spectral data
`x,object`	Object to be converted to or from Speclib. For conversion to Speclib it can be a of class `'data frame'`, `'matrix'`, `'list'` or `'character string'`. In the latter case x is interpreted as path to raster object and read by `readGDAL`. For conversion from `Speclib` the object must be of class `Speclib`.
`wavelength`	Vector with corresponding wavelength for each band. A matrix or data.frame may be passed giving the upper and lower limit of each band. In this case, the first column is used as lower band limit and the second as upper limit, respectively.
`fwhm`	Vector containing full-width-half-max values for each band
`attributes`	Data frame with additional attributes data.
`transformation`	Kind of transformation applied to spectral data (character)
`usagehistory`	Character string or vector used for history of usage
`continuousdata`	Flag indicating if spectra are quasi continuous or discrete sensor spectra
`wlunit`	Unit of wavelength in spectra
`xlabel`	Label of wavelength data to be used for plots etc.
`ylabel`	Label of spectral signal to be used for plots etc.
`rastermeta`	List of meta information for SpatialGridDataFrame or HyperSpecRaster. If missing, meta data in speclib is used. Use function `rastermeta` to create valid objects.
`...`	Further arguments passed to specific (generic) functions or createspeclib

Details

See details in `Speclib`.

Value

An object of class `Speclib` containing the following slots is returned:

- wavelength: Vector with wavelength information
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- spectra: Object of class '.Spectra' with three slots:
  - fromRaster: logical, indicating if spectral data is read from a RasterBrick-object.
  - spectra_ma: Matrix with ncol = number of bands and nrow = number. Used if fromRaster == FALSE

  – spectra_ra: RasterBrick-object which is used if fromRaster == TRUE.

  Contains reflectance, transmittance or absorbance values. Handle with function `spectra`.

- attributes: Data frame containing additional data to each spectrum. May be used for linear regression etc. Handle with function `attribute`.
- usagehistory: Vector giving information on history of usage of speclib. Handle with function `usagehistory`.
- rastermeta: List containing meta information to create *Raster objects from Speclib. Handle with function `rastermeta`.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `plot`, `readGDAL`, `mask`,

`idSpeclib`, `dim`, `spectra`,

`attribute`

Examples

```
data(spectral_data)
spectra <- spectra(spectral_data)
wavelength <- spectral_data$wavelength

spectra <- speclib(spectra,wavelength)
```

Speclib-class ** Speclib class*

Description

Class to store and handle hyperspectral data in R

Details

Spectral data: The spectral data (usually reflectance values) are stored in an object of class `'.Spectra'`. This object may eiter contain the spectral data as a `RasterBrick` or as a `matrix` with columns indicating spectral bands and rows different samples, respectively. The Speclib-class provides converting routines to and from `RasterBrick`-class allowing to read and write geographic raster data via `brick` and its extension `HyperSpecRaster-class`. Since R is in general not intended to be used for VERY large data sets, this functionality should be handled with care. If raster files are large, one should split them in multiple smaller ones and process each of the small files, separately. See the excellent tutorial 'Writing functions for large raster files' available on https://cran.r-project.org/web/packages/raster/vignettes/functions.pdf and section '2.2.2 Speclibs from raster files' in 'hsdar-intro.pdf'.

Spectral information: Speclib contains wavelength information for each band in spectral data. This information is used for spectral resampling, vegetation indices and plotting etc. Since spectra can be handled either as continuous lines or as discrete values like for satellite bands, spectral information is handled in two principle ways:

- Continuous spectra: Data of spectrometers or hyperspectral (satellite) sensors. This data is plotted as lines with dotted lines indicating standard deviations by default.
- Non-continuous spectra: Data of multispectral satellite sensors. Here, data is plotted as solid lines and error bars at the mean position of each waveband indicating standard deviations by default.

The kind of data may be chosen by the user by setting the attribute flag `"continuousdata"` (`attr(x, "continuousdata")`) or passing `continuousdata = TRUE/FALSE`, when initially converting data to `Speclib`-class. Take care of doing so, because some functions as `spectralResampling` may only work correctly with continuous data!

The unit of spectral data must be set initially, when converting data to speclib. Note that the package currently supports only "nm" as unit. This is particularly important for function like `vegindex`, which need to get correct bands out of the spectral data.

Technical description: An object of class `Speclib` contains the following slots:

- wavelength: Vector with wavelength information.
- fwhm: Vector or single numerical value giving the full-width-half-max value(s) for each band.
- spectra: Object of class '.Spectra' with three slots:
  - fromRaster: logical, indicating if spectral data is read from a RasterBrick-object.
  - spectra_ma: Matrix with ncol = number of bands and nrow = number. Used if fromRaster == FALSE
  - spectra_ra: RasterBrick-object which is used if fromRaster == TRUE.

  Contains reflectance, transmittance or absorbance values. Handle with function `spectra`.
- attributes: Data frame containing additional data to each spectrum. May be used for linear regression etc. Handle with function `attribute`.
- usagehistory: Vector giving information on history of usage of speclib. Handle with function `usagehistory`.

Note

See figure in `hsdar-package` for an overview of classes in hsdar.

Author(s)

Lukas Lehnert

See Also

`plot`, `readGDAL`, `mask`, `idSpeclib`,

`dim`, `spectra`, `attribute`

spectra *Handling spectra*

Description

Returning and setting spectra in Speclib

Usage

```
## S4 method for signature 'Speclib'
spectra(object, i, j, ...)

## S4 replacement method for signature 'Speclib,data.frame'
spectra(object) <- value

## S4 replacement method for signature 'Speclib,matrix'
spectra(object) <- value

## S4 replacement method for signature 'Speclib,numeric'
spectra(object) <- value

## S4 replacement method for signature 'Speclib,RasterBrick'
spectra(object) <- value
```

Arguments

`object`	Object of class `Speclib`.
`i`	Index of spectra to return. If missing all spectra are returned.
`j`	Index of bands to return. If missing all bands are returned.
`...`	Passed to internal function. Currently only one parameter is accepted: `return_names`: Logical indicating, if names of columns and rows should be set to `bandnames` and `idSpeclib`.
`value`	Matrix or RasterBrick-object containing spectral values. If value is a matrix, columns are band values and rows are spectra.

Details

For `spectra<-`, the function does not check if dimensions of spectra match dimensions of Speclib. Additionally, no conversion into `matrix` is performed! If spectra are not correctly stored, errors in other functions may arise. Thus check always carefully, if spectra are modified by hand.

Value

For `spectra<-`, the updated object. Otherwise a matrix of the spectra in x is returned.

Author(s)

Lukas Lehnert

See Also

`Speclib`

Examples

```
data(spectral_data)

## Manual plot of the first spectrum
plot(wavelength(spectral_data), spectra(spectral_data)[1,], type="l")
```

---

spectralResampling *Spectral resampling*

Description

Resample spectra to (satellite) sensors

Usage

```
spectralResampling(x, sensor, rm.NA = TRUE, continuousdata = "auto",
                   response_function = TRUE)
```

Arguments

`x`	Object of class `Speclib`. Data to be spectrally resampled.
`sensor`	Character or `data.frame` containing definition of sensor characteristics. See details section for further information.
`rm.NA`	If `TRUE`, channels which are not covered by input data wavelength are removed
`continuousdata`	Definition if returned `Speclib` is containing continuous data or not.
`response_function`	If `TRUE`, the spectral response function of the sensor is used for integration, if `FALSE` a Gaussian distribution is assumed and if `NA` the mean value of `spectra[min(ch):max(ch)]` is calculated.

Details

The characteristics of (satellite) sensor to integrate spectra can be chosen from a list of already implemented sensors. See `get.sensor.characteristics` for available sensors.

Otherwise the characteristics can be passed as a `data.frame` with two columns: first column with lower bounds of channels and second column with upper bounds. Alternatively, the `data.frame` may encompass band centre wavelength and full-width-half-maximum values of the sensor. Function will check the kind of data passed by partially matching the names of the data frame: If any column is named "fwhm" or "center", it is assumed that data are band centre and full-width-half-maximum values.

If sensor characteristics are defined manually, a Gaussian response is always assumed.

Value

Object of class Speclib

Author(s)

Lukas Lehnert

See Also

get.sensor.characteristics, get.gaussian.response

Examples

```
## Load example data
data(spectral_data)

## Resample to RapidEye
data_RE <- spectralResampling(spectral_data, "RapidEye",
                              response_function = TRUE)

## Plot resampled spectra
plot(data_RE)

## Compare different methods of spectral resampling
par(mfrow=c(1,3))
ga <- spectralResampling(spectral_data, "RapidEye",
                         response_function = FALSE)
plot(ga)
re <- spectralResampling(spectral_data, "RapidEye",
                         response_function = TRUE)
plot(re)
no <- spectralResampling(spectral_data, "RapidEye",
                         response_function = NA)
plot(no)
```

---

spectral_data *Hyperspectral samples*

Description

Hyperspectral samples from a FACE experiment in Germany

Usage

```
data(spectral_data)
```

Format

An object of class `Speclib`

Details

Data has been sampled during vegetation period 2014 in spring and summer. Measurements were taken with a HandySpec Field portable spectrometer (tec5 AG Oberursel, Germany). This device has two channels measuring incoming and reflected radiation simultaneously between 305 and 1705 nm in 1 nm steps.

Author(s)

Wolfgang A. Obermeier, Lukas Lehnert, Hanna Meyer

---

subset.nri *Subsetting* `Nri`*-objects*

Description

Return subsets of `Nri`-objects which meet conditions.

Usage

```
## S4 method for signature 'Nri'
subset(x, subset, ...)
```

Arguments

`x`	Object of class 'Nri'.
`subset`	Logical expression indicating spectra to keep: missing values are taken as false. See details section.
`...`	Further arguments passed to `agrep`.

Details

Matchable objects are attributes data. Use column names to identify the respectrive attribute. See `attribute` to access attributes of a `Nri`. IDs of samples may be accessed using "id.nri" as variable name.

Value

Object of class `Nri`.

Author(s)

Lukas Lehnert

See Also

Nri, attribute

Examples

```
data(spectral_data)

## Calculate all possible combinations for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Return names of attributes data
names(attribute(nri_WV))

## Devide into both seasons
sp_summer <- subset(nri_WV, season == "summer")
sp_spring <- subset(nri_WV, season == "spring")

## Print both Nri-objects
sp_summer
sp_spring
```

---

subset.speclib *Subsetting speclibs*

Description

Return subsets of Speclibs which meet conditions.

Usage

```
## S4 method for signature 'Speclib'
subset(x, subset, ...)
```

Arguments

x	Object of class 'Speclib'.
subset	Logical expression indicating spectra to keep: missing values are taken as false. See details section.
...	Further arguments passed to agrep.

Details

Matchable objects are attributes data. Use column names to identify the respectrive attribute. See `attribute` to access attributes of a `Speclib`. IDs of spectra may be accessed using "id.speclib" as variable name.

Value

Object of class `Speclib`.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `attribute`

Examples

```
data(spectral_data)

## Return names of attributes data
names(attribute(spectral_data))

## Devide into both seasons
sp_summer <- subset(spectral_data, season == "summer")
sp_spring <- subset(spectral_data, season == "spring")

## Plot both speclibs
plot(sp_summer, col="darkgreen")
plot(sp_spring, col="darkred", new=FALSE)
```

---

t.test *t-test for nri values*

Description

Performs t-tests for nri values.

Usage

```
## S4 method for signature 'Nri'
t.test(x, ...)
```

Arguments

`x`	Object of class 'nri'.
`...`	Arguments to be passed to `t.test`.

Value

An object of class "data.frame"

Author(s)

Lukas Lehnert & Hanna Meyer

See Also

`t.test`, `cor.test`, `Nri-method`

Examples

```
data(spectral_data)


## Calculate nri-values for WorldView-2-8
spec_WV <- spectralResampling(spectral_data, "WorldView2-8",
                              response_function = FALSE)
nri_WV <- nri(spec_WV, recursive = TRUE)

## Perform t.tests between nri-values of both sites
season <- spec_WV$attributes$season
ttestres <- t.test(x = nri_WV, y = season, alternative = "two.sided")
ttestres

## Plot p.values of t.tests
plot(ttestres)
```

`transformSpeclib` *Transform spectra*

Description

Transform spectra by using convex hull or segmented upper hull

Usage

```
transformSpeclib(data, ..., method = "ch", out = "bd")
```

Arguments

`data`	Speclib to be transformed
`method`	Method to be used. See details section.
`out`	Kind of value to be returned. See details section.
`...`	Further arguments passed to generic functions. Currently ignored.

Details

Function performs a continuum removal transformation by firstly establishing a continuum line/hull which connects the local maxima of the reflectance spectrum. Two kinds of this hull are well established in scientific community: the convex hull (e.g. Mutanga et al. 2004) and the segmented hull (e.g. Clark et al. 1987). Both hulls are established by connecting the local maxima, however, the precondition of the convex hull is that the resulting continuum line must be convex whereas considering the segmented hull it might be concave or convex but the algebraic sign of the slope is not allowed to change from the global maximum of the spectrum downwards to the sides. In contrast to a convex hull, the segmented hull is able to identify small absorption features.

Specify `method = "ch"` for the convex hull and `method = "sh"` for the segmented hull. The output might be `"raw"`, `"bd"` or `"ratio"`:

- "raw": the continuum line is returned
- "bd": the spectra are transformed to band depth by

  $$BD_\lambda = 1 - \frac{R_\lambda}{CV_\lambda},$$

  where BD is the band depth, R is the reflectance and CV is the continuum value at the wavelength λ.
- "ratio": the spectra are transformed by

  $$BD_\lambda = \frac{R_\lambda}{CV_\lambda}.$$

In some cases it might be useful to apply `smoothSpeclib` before the transformation if too many small local maxima are present in the spectra. Anyway, a manual improvement of the continuum line is possible using `addcp` and `deletecp`.

Value

If `method != "raw"` an object of class `Speclib` containing transformed spectra is returned. Otherwise the return object will be of class `Clman`.

Author(s)

Hanna Meyer and Lukas Lehnert

References

Clark, R. N., King, T. V. V. and Gorelick, N. S. (1987): Automatic continuum analysis of reflectance spectra. Proceedings of the Third Airborne Imaging Spectrometer Data Analysis Workshop, 30. 138-142.

Mutanga, O. and Skidmore, A. K. (2004): Hyperspectral band depth analysis for a better estimation of grass biomass (Cenchrus ciliaris) measured under controlled laboratory conditions International Journal of applied Earth Observation and Geoinformation, 5, 87-96.

See Also

`Clman`, `addcp`, `deletecp`, `checkhull`

Examples

```
data(spectral_data)

transformed_spectra <- transformSpeclib(spectral_data)

par(mfrow=c(1,2))
plot(spectral_data)
plot(transformed_spectra)
```

`unmix` *Unmix spectra*

Description

Unmix spectra or spectra resampled to satellite bands using endmember spectra

Usage

```
unmix(spectra, endmember, returnHCR = "auto", scale = FALSE, ...)
```

Arguments

`spectra`	Input spectra of class 'speclib'
`endmember`	Endmember spectra of class 'speclib'
`returnHCR`	Set class of value. If TRUE, value will be of class '`HyperSpecRaster`', otherwise a list is returned. If `auto`, function will switch to mode depending on input data characteristics.
`scale`	Flag to scale spectra to [0,1] if necessary.
`...`	Further arguments passed to `HyperSpecRaster` (ignored if returnHCR = FALSE).

Details

Linear spectral unmixing is a frequently used method to calculate fractions of land-cover classes (endmembers) within the footprint of pixels. This approach has originally been intended to be used for multispectral satellite images. The basic assumption is that the signal received at the sensor (ρ_{mix}) is a linear combination of n pure endmember signals (ρ_i) and their cover fractions (f_i):

$$\rho_{mix} = \sum_{i=1}^{n} \rho_i f_i,$$

where $f_1, f_2, ..., f_n >= 0$ and $\sum_{i=1}^{n} f_i = 1$ to fulfill two constraints:

1. All fractions must be greater or equal 0
2. The sum of all fractions must be 1

Since this linear equation system is usually over-determined, a least square solution is performed. The error between the final approximation and the observed pixel vector is returned as vector (`error`) in list (`returnSpatialGrid = FALSE`) or as last band if `returnSpatialGrid = TRUE`.

Value

A list containing the fraction of each endmember in each spectrum and an error value giving the euclidean norm of the error vector after least square error minimisation.

Note

Unmixing code is based on "i.spec.unmix" for GRASS 5 written by Markus Neteler (1999).

Author(s)

Lukas Lehnert

References

Sohn, Y. S. & McCoy, R. M. (1997): Mapping desert shrub rangeland using spectral unmixing and modeling spectral mixtures with TM data. Photogrammetric Engineering and Remote Sensing, 63, 707-716

Examples

```
## Not run:
## Use PROSAIL to generate some vegetation spectra with different LAI
parameter <- data.frame(LAI = seq(0, 1, 0.01))
spectral_data <- PROSAIL(parameterList = parameter)

## Get endmember spectra
## Retrieve all available spectra
avl <- USGS_get_available_files()

## Download all spectra matching "grass-fescue"
grass_spectra <- USGS_retrieve_files(avl = avl, pattern = "grass-fescue")
```

```
limestone <- USGS_retrieve_files(avl = avl, pattern = "limestone")

## Integrate all spectra to Quickbird
grass_spectra_qb <- spectralResampling(grass_spectra[1,], "Quickbird")
limestone_qb <- spectralResampling(limestone, "Quickbird")
spectral_data_qb <- spectralResampling(spectral_data, "Quickbird")


em <- speclib(spectra = rbind(spectra(grass_spectra_qb),
                              spectra(limestone_qb))/100,
              wavelength = wavelength(limestone_qb))

## Unmix
unmix_res <- unmix(spectral_data_qb, em)

unmix_res

plot(unmix_res$fractions[1,] ~ attribute(spectral_data_qb)$LAI, type = "l",
     xlab = "LAI", ylab = "Unmixed fraction of vegetation")

## End(Not run)
```

`updatecl` *Check continuum line*

Description

Check if continuum line is intersecting the reflectance curve.

Usage

```
updatecl(x, hull)
```

Arguments

`x`	Object of class `Speclib` transformed by `transformSpeclib`.
`hull`	Hull to be applied to x. Output of function `makehull`.

Value

Object of class `Speclib`.

Author(s)

Lukas Lehnert and Hanna Meyer

See Also

`transformSpeclib`, `makehull`, `Speclib`

Examples

```
## Model spectra using PROSAIL
parameter <- data.frame(N = rep.int(c(1, 1.5),2), LAI = c(1,1,3,3))
spec <- PROSAIL(parameterList=parameter)

## Transform spectra
spec_clman <- transformSpeclib(spec, method = "sh", out = "raw")

## Plot original line
par(mfrow = c(1,2))
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Add fix point at 4595 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2495)

## Plot new line
plot(spec_clman, ispec = 1, subset = c(2480, 2500))

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

## Add fix point at 4596 nm to continuum line of first spectrum
spec_clman <- addcp(spec_clman, 1, 2496)

## Check new hull
hull <- checkhull(spec_clman, 1)
hull$error

hull <- makehull(spec_clman, 1)

## Transform spectra using band depth
spec_bd <- transformSpeclib(spec, method = "sh", out = "bd")

## Update continuum line of first spectrum
spec_bd <- updatecl(spec_bd, hull)

## Plot modified transformed spectrum
plot(spec_bd, FUN = 1)
```

`usagehistory` *History of usage*

Description

Handling history of usage of Speclibs

Usage

```
usagehistory(x)
usagehistory(x) <- value
```

Arguments

x	Object of class Speclib
value	Character string to be added to usagehistory or NULL, if usagehistory should be deleted.

Value

For `usagehistory<-`, the updated object. Otherwise a vector giving the history of usage of Speclib is returned.

Author(s)

Lukas Lehnert

See Also

Speclib

Examples

```
data(spectral_data)

## Return history of usage
usagehistory(spectral_data)

## Deleting history of usage
usagehistory(spectral_data) <- character()
spectral_data

## Adding entries
usagehistory(spectral_data) <- "New entry" ## Adding new entry
usagehistory(spectral_data) <- "New entry 2" ## Adding second entry
spectral_data
```

---

vegindex *vegindex*

Description

Function calculates a variety of hyperspectral vegetation indices

Usage

```
vegindex(x, index, returnHCR = "auto", L = 0.5,
         weighted = TRUE, ...)
```

Arguments

`x`	Object of class `Speclib`
`index`	Character string. Name or definition of index or vector with names/definitions of indices to calculate. See Details section for further information.
`returnHCR`	If TRUE, the result will be of class HyperSpecRaster, otherwise it is a data frame. If "auto", the class is automatically determined by passed Speclib.
`L`	Factor for SAVI index. Unused for other indices.
`weighted`	Logical indicating if reflectance values should be interpolated to fit wavelength position. If `FALSE` the reflectance values of nearest neighbour to passed position are returned. See `get_reflectance` for further explanation.
`...`	Further arguments passed to derivative functions. Only used for indices requiring derivations.

Details

Index must be a charater vector containing pre-defined indices (selected by their name) or self defined indices or any combination of pre- and self-defined indices.

Pre-defined indices: The following indices are available:

Name	**Formula**	**Reference***
Boochs	D_{703}	Boochs et al. (1990)
Boochs2	D_{720}	Boochs et al. (1990)
CAI	$0.5 \cdot (R_{2000} + R_{2200}) - R_{2100}$	Nagler et al. (2003)
CARI	$a = (R_{700} - R_{550})/150$ $b = R_{550} - (a \cdot 550)$ $R_{700} \cdot \text{abs}(a \cdot 670 + R_{670} + b)/R_{670} \cdot$ $(a^2 + 1)^{0.5}$	Kim et al. (1994)
Carter	R_{695}/R_{420}	Carter (1994)
Carter2	R_{695}/R_{760}	Carter (1994)
Carter3	R_{605}/R_{760}	Carter (1994)
Carter4	R_{710}/R_{760}	Carter (1994)
Carter5	R_{695}/R_{670}	Carter (1994)
Carter6	R_{550}	Carter (1994)
CI	$R_{675} \cdot R_{690}/R_{683}^2$	Zarco-Tejada et al. (2003)
CI2	$R_{760}/R_{700} - 1$	Gitelson et al. (2003)
ClAInt	$\int_{600nm}^{735nm} R$	Oppelt and Mauser (2004)
CRI1	$1/R_{515} - 1/R_{550}$	Gitelson et al. (2003)
CRI2	$1/R_{515} - 1/R_{770}$	Gitelson et al. (2003)
CRI3	$1/R_{515} - 1/R_{550} \cdot R_{770}$	Gitelson et al. (2003)
CRI4	$1/R_{515} - 1/R_{700} \cdot R_{770}$	Gitelson et al. (2003)
D1	D_{730}/D_{706}	Zarco-Tejada et al. (2003)

D2	D_{705}/D_{722}	Zarco-Tejada et al. (2003)
Datt	$(R_{850} - R_{710})/(R_{850} - R_{680})$	Datt (1999b)
Datt2	R_{850}/R_{710}	Datt (1999b)
Datt3	D_{754}/D_{704}	Datt (1999b)
Datt4	$R_{672}/(R_{550} \cdot R_{708})$	Datt (1998)
Datt5	R_{672}/R_{550}	Datt (1998)
Datt6	$(R_{860})/(R_{550} \cdot R_{708})$	Datt (1998)
Datt7	$(R_{860} - R_{2218})/(R_{860} - R_{1928})$	Datt (1999a)
Datt8	$(R_{860} - R_{1788})/(R_{860} - R_{1928})$	Datt (1999a)
DD	$(R_{749} - R_{720}) - (R_{701} - R_{672})$	le Maire et al. (2004)
DDn	$2 \cdot (R_{710} - R_{660} - R_{760})$	le Maire et al. (2008)
DPI	$(D_{688} \cdot D_{710})/D_{697}^2$	Zarco-Tejada et al. (2003)
DWSI1	R_{800}/R_{1660}	Apan et al. (2004)
DWSI2	R_{1660}/R_{550}	Apan et al. (2004)
DWSI3	R_{1660}/R_{680}	Apan et al. (2004)
DWSI4	R_{550}/R_{680}	Apan et al. (2004)
DWSI5	$(R_{800} + R_{550})/(R_{1660} + R_{680})$	Apan et al. (2004)
EGFN	$(\max(D_{650:750}) - \max(D_{500:550}))/(\max(D_{650:750}) + \max(D_{500:550}))$	Penuelas et al. (1994)
EGFR	$\max(D_{650:750})/\max(D_{500:550})$	Penuelas et al. (1994)
EVI	$2.5 \cdot ((R_{800} - R_{670})/(R_{800} - (6 \cdot R_{670}) - (7.5 \cdot R_{475}) + 1))$	Huete et al. (1997)
GDVI	$(R_{800}^n - R_{680}^n)/(R_{800}^n + R_{680}^n)$**	Wu (2014)
GI	R_{554}/R_{677}	Smith et al. (1995)
Gitelson	$1/R_{700}$	Gitelson et al. (1999)
Gitelson2	$(R_{750} - R_{800}/R_{695} - R_{740}) - 1$	Gitelson et al. (2003)
GMI1	R_{750}/R_{550}	Gitelson et al. (2003)
GMI2	R_{750}/R_{700}	Gitelson et al. (2003)
Green NDVI	$(R_{800} - R_{550})/(R_{800} + R_{550})$	Gitelson et al. (1996)
LWVI_1	$(R_{1094} - R_{983})/(R_{1094} + R_{983})$	Galvao et al. (2005)
LWVI_2	$(R_{1094} - R_{1205})/(R_{1094} + R_{1205})$	Galvao et al. (2005)
Maccioni	$(R_{780} - R_{710})/(R_{780} - R_{680})$	Maccioni et al. (2001)
MCARI	$((R_{700} - R_{670}) - 0.2 \cdot (R_{700} - R_{550})) \cdot (R_{700}/R_{670})$	Daughtry et al. (2000)
MCARI/OSAVI		Daughtry et al. (2000)
MCARI2	$((R_{750} - R_{705}) - 0.2 \cdot (R_{750} - R_{550})) \cdot (R_{750}/R_{705})$	Wu et al. (2008)
MCARI2/OSAVI2		Wu et al. (2008)
mND705	$(R_{750} - R_{705})/(R_{750} + R_{705} - 2 \cdot R_{445})$	Sims and Gamon (2002)
mNDVI	$(R_{800} - R_{680})/(R_{800} + R_{680} - 2 \cdot R_{445})$	Sims and Gamon (2002)
MPRI	$(R_{515} - R_{530})/(R_{515} + R_{530})$	Hernandez-Clemente et al. (2011)
mREIP	Red-edge inflection point using Gaussain fit	Miller et al. (1990)
MSAVI	$0.5 \cdot (2 \cdot R_{800} + 1 - ((2 \cdot R_{800} + 1)^2 - 8 \cdot (R_{800} - R_{670}))^{0.5})$	Qi et al. (1994)
MSI	R_{1600}/R_{817}	Hunt and Rock (1989)

mSR	$(R_{800} - R_{445})/(R_{680} - R_{445})$	Sims and Gamon (2002)
mSR2	$(R_{750}/R_{705}) - 1/(R_{750}/R_{705} + 1)^{0.5}$	Chen (1996)
mSR705	$(R_{750} - R_{445})/(R_{705} - R_{445})$	Sims and Gamon (2002)
MTCI	$(R_{754} - R_{709})/(R_{709} - R_{681})$	Dash and Curran (2004)
MTVI	$1.2 \cdot (1.2 \cdot (R_{800} - R_{550}) -$ $2.5 \cdot (R_{670} - R_{550}))$	Haboudane et al. (2004)
NDLI	$(log(1/R_{1754}) - log(1/R_{1680}))/$ $(log(1/R_{1754}) + log(1/R_{1680}))$	Serrano et al. (2002)
NDNI	$(log(1/R_{1510}) - log(1/R_{1680}))/$ $(log(1/R_{1510}) + log(1/R_{1680}))$	Serrano et al. (2002)
NDVI	$(R_{800} - R_{680})/(R_{800} + R_{680})$	Tucker (1979)
NDVI2	$(R_{750} - R_{705})/(R_{750} + R_{705})$	Gitelson and Merzlyak (1994)
NDVI3	$(R_{682} - R_{553})/(R_{682} + R_{553})$	Gandia et al. (2004)
NDWI	$(R_{860} - R_{1240})/(R_{860} + R_{1240})$	Gao (1996)
NPCI	$(R_{680} - R_{430})/(R_{680} + R_{430})$	Penuelas et al. (1994)
OSAVI	$(1 + 0.16) \cdot (R_{800} - R_{670})/$ $(R_{800} + R_{670} + 0.16)$	Rondeaux et al. (1996)
OSAVI2	$(1 + 0.16) \cdot (R_{750} - R_{705})/$ $(R_{750} + R_{705} + 0.16)$	Wu et al. (2008)
PARS	R_{746}/R_{513}	Chappelle et al. (1992)
PRI	$(R_{531} - R_{570})/(R_{531} + R_{570})$	Gamon et al. (1992)
PRI_norm	PRI $\cdot (-1)/($RDVI $\cdot R_{700}/R_{670})$	Zarco-Tejada et al. (2013)
PRI*CI2	PRI $\cdot$ CI2	Garrity et al. (2011)
PSRI	$(R_{678} - R_{500}/R_{750}$	Merzlyak et al. (1999)
PSSR	R_{800}/R_{635}	Blackburn (1998)
PSND	$(R_{800} - R_{470})/(R_{800} - R_{470})$	Blackburn (1998)
PWI	R_{970}/R_{900}	Penuelas et al. (1997)
RDVI	$(R_{800} - R_{670})/\sqrt{R_{800} + R_{670}}$	Roujean and Breon (1995)
REP_LE	Red-edge position through linear extrapolation.	Cho and Skidmore (2006)
REP_Li	$R_{re} = (R_{670} + R_{780})/2$ $700 + 40 \cdot ((R_{re} - R_{700})/(R_{740} - R_{700}))$	Guyot and Baret (1988)
SAVI	$(1 + L) \cdot (R_{800} - R_{670})/(R_{800} + R_{670} + L)$	Huete (1988)
SIPI	$(R_{800} - R_{445})/(R_{800} - R_{680})$	Penuelas et al. (1995), Penuelas et al. (1995a)
SPVI	$0.4 \cdot 3.7 \cdot (R_{800} - R_{670}) - 1.2 \cdot$ $((R_{530} - R_{670})^2)^{0.5}$	Vincini et al. (2006)
SR	R_{800}/R_{680}	Jordan (1969)
SR1	R_{750}/R_{700}	Gitelson and Merzlyak (1997)
SR2	R_{752}/R_{690}	Gitelson and Merzlyak (1997)
SR3	R_{750}/R_{550}	Gitelson and Merzlyak (1997)
SR4	R_{700}/R_{670}	McMurtey et al. (1994)
SR5	R_{675}/R_{700}	Chappelle et al. (1992)
SR6	R_{750}/R_{710}	Zarco-Tejada and Miller

		(1999)
SR7	R_{440}/R_{690}	Lichtenthaler et al. (1996)
SR8	R_{515}/R_{550}	Hernandez-Clemente et al. (2012)
SRPI	R_{430}/R_{680}	Penuelas et al. (1995)
SRWI	R_{850}/R_{1240}	Zarco-Tejada et al. (2003)
Sum_Dr1	$\sum_{i=626}^{795} D1_i$	Elvidge and Chen (1995)
Sum_Dr2	$\sum_{i=680}^{780} D1_i$	Filella and Penuelas (1994)
SWIR FI	$R_{2133}^2/(R_{2225} \cdot R_{2209}^3$	Levin et al. (2007)
SWIR LI	$3.87 \cdot (R_{2210} - R_{2090}) - 27.51 \cdot (R_{2280} - R_{2090}) - 0.2$	Lobell et al. (2001)
SWIR SI	$-41.59 \cdot (R_{2210} - R_{2090}) + 1.24 \cdot (R_{2280} - R_{2090}) + 0.64$	Lobell et al. (2001)
SWIR VI	$37.72 \cdot (R_{2210} - R_{2090}) + 26.27 \cdot (R_{2280} - R_{2090}) + 0.57$	Lobell et al. (2001)
TCARI	$3 \cdot ((R_{700} - R_{670}) - 0.2 \cdot (R_{700} - R_{550}) \cdot (R_{700}/R_{670}))$	Haboudane et al. (2002)
TCARI/OSAVI	$\mathrm{TCARI}/\mathrm{OSAVI}$	Haboudane et al. (2002)
TCARI2	$3 \cdot ((R_{750} - R_{705}) - 0.2 \cdot (R_{750} - R_{550}) \cdot (R_{750}/R_{705}))$	Wu et al. (2008)
TCARI2/OSAVI2	$\mathrm{TCARI2}/\mathrm{OSAVI2}$	Wu et al. (2008)
TGI	$-0.5(190(R_{670} - R_{550}) - 120(R_{670} - R_{480}))$	Hunt et al. (2013)
TVI	$0.5 \cdot (120 \cdot (R_{750} - R_{550}) - 200 \cdot (R_{670} - R_{550}))$	Broge and Leblanc (2000)
Vogelmann	R_{740}/R_{720}	Vogelmann et al. (1993)
Vogelmann2	$(R_{734} - R_{747})/(R_{715} + R_{726})$	Vogelmann et al. (1993)
Vogelmann3	D_{715}/D_{705}	Vogelmann et al. (1993)
Vogelmann4	$(R_{734} - R_{747})/(R_{715} + R_{720})$	Vogelmann et al. (1993)

* For references please type: `hsdardocs("References.pdf")`.
** For GDVI n must be defined appending an underscore and the intended exponent to the index name. E.g., for n = 2, the correct index name would be "GDVI_2". Note that GDVI-indices with n = 2, 3, 4 will be derived if all available indices are calculated.

Self-defining indices:

Self-defined indices may be passed using the following syntax:

- Rxxx: Reflectance at wavelength 'xxx'. Note that R must be upper case.
- Dxxx: First derivation of reflectance values at wavelength 'xxx'. Note that D must be upper case.

Using this syntax, complex indices can be easily defined. Note that the entire definition of the index must be passed as one character string. Consequently, the NDVI would be written as "(R800-R680)/(R800+R680)".

Value

A vector containing indices values. If index is a vector with length > 1, a data frame with ncol = length(index) and nrow = number of spectra in x is returned.

If function is called without any arguments, return value will be a vector containing all available indices in alphabetical order.

Author(s)

Hanna Meyer and Lukas Lehnert

References

See hsdardocs("References.pdf")

See Also

soilindex, derivative.speclib, rededge, get_reflectance

Examples

```
## Example calculating NDVI
data(spectral_data)
ndvi <- vegindex(spectral_data, "NDVI")


## Example calculating all available indices
## Get available indices
avl <- vegindex()
vi <- vegindex(spectral_data, avl)

## Self-defined indices
## NDVI
vi <- vegindex(spectral_data, "(R800-R680)/(R800+R680)")
## NDNI
vi <- vegindex(spectral_data,
               "(log(1/R1510) - log(1/R1680))/(log(1/R1510) + log(1/R1680))")
## D1
vi <- vegindex(spectral_data, "D730/D706")
```

---

wavelength *Handling wavelength and fwhm*

Description

Returning and setting wavelength and full-width-half-max (fwhm) values in Speclib and HyperSpecRaster

Usage

```
## S4 method for signature 'Speclib'
wavelength(object)

## S4 replacement method for signature 'Speclib,data.frame'
wavelength(object) <- value

## S4 replacement method for signature 'Speclib,numeric'
wavelength(object) <- value

## S4 method for signature 'HyperSpecRaster'
wavelength(object)

## S4 replacement method for signature 'HyperSpecRaster,numeric'
wavelength(object) <- value

## S4 method for signature 'Speclib'
fwhm(object)

## S4 replacement method for signature 'Speclib,numeric'
fwhm(object) <- value
```

Arguments

`object`	Object of class `Speclib` or `HyperSpecRaster`.
`value`	Numeric vector or data.frame containing wavelength values.

Value

For `wavelength<-` and `fwhm<-`, the updated object. Otherwise a numeric vector of the wavelength and fwhm-values is returned.

Author(s)

Lukas Lehnert

See Also

`Speclib`, `HyperSpecRaster`

Examples

```
data(spectral_data)

wavelength(spectral_data)
```

Index